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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:

May 29, 2003, 08:39:22; Search time 49 Seconds (without alignments)
2056.099 Million cell updates/sec

Title:

US-10-031-146-2
Perfect score:
1048
Sequence:
1 TIKEMPQPKTFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048
Scoring table: OLIGO
Gapop 60.0, Gapext 60.0
Searched:
283224 seqs, 96134422 residues
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Post-processing: Listing first 45 summaries

283224

Total number of hits satisfying chosen parameters:

0

Word size :

seq length: 0 seq length: 2000000000

Minimum DB : Maximum DB : Post\_processing: Listing ille
Database: PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

nitric-oxide synth	nitric-oxide synth	ferredoxin-NADP re	ferredoxin-NADP re	probable ferredoxi	probable cytochrom	NADPH-ferrihemopro	NADPH-ferrihemopro	NADPH-ferrihemopro	NADPH-ferrihemopro	NADPH-ferrihemopro	nitric-oxide synth	nitric-oxide synth	nitric-oxide synth	nitric-oxide synth	nitric-oxide synth
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S16233	G01946	<b>S53305</b>	T02215	T03758	T06715	A56592	<b>S63895</b>	863638	A37890	T10723	A43271	S47647	156575	838253	153165
7	7	~	~	Н	~	7	~	N	7	~	Н	٦	Н	-	н
1429	1433	327	375	378	489	671	680	680	680	705	1144	1147	1147	1147	1147
1.0	1.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	0.9	6.0
10	10	σ	0	6	σ	σ	6	O	0	6	6	9	σ	6	6
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
	1429 2 S16233 . n	1429 2 S16233 n 1433 2 G01946	1429 2 S16233 n 1433 2 G01946 n 327 2 S53305 f	1429 2 S16233 1433 2 G01946 375 2 F02215	1429 2 S16233 1433 2 G01946 327 2 S53305 375 2 T02215 378 1 T03758	1429 2 S16233 1433 2 G01946 327 2 S53305 375 2 T02215 378 1 T03758 489 2 T06715	1429 2 S16233 1433 2 G01946 327 2 S53305 375 2 T02215 378 1 T03758 489 2 T06715 671 2 A56592	1429 2 \$16233	1429 2 \$16233 1433 2 \$601946 327 2 \$53305 375 2 T02215 378 1 T02758 479 2 T06715 671 2 A56592 680 2 \$63895	1429 2 \$16233 1433 2 \$61046 327 2 \$5305 378 1 702015 671 2 A56595 680 2 \$63895 680 2 \$63895 680 2 \$73598	1429 2 S16233 1433 2 G01046 327 2 S5305 375 2 T02215 378 1 T03758 489 2 T06715 680 2 S6592 680 2 S63895 680 2 A37890 705 2 T10723	1429 2 \$16233 1433 2 \$601946 327 2 \$53305 375 2 T02215 378 1 T02758 479 2 T06715 671 2 A56592 680 2 \$63895 680 2 \$63898 680 2 A37890 705 2 T10723	1429 2 \$16233 1433 2 \$61046 327 2 \$53055 378 1 702758 489 2 706715 671 2 A56592 680 2 \$63895 680 2 \$63895 680 2 \$73890 705 2 \$10723 1147 1 \$47647	1429 2 516233 nitric-oxide 1433 2 601946 nitric-oxide 1433 2 55305 ferredoxin-NJ 375 2 702215 probable ferredoxin-NJ 378 1 703758 probable ferredoxin-NJ 2 A56592 NADPH-ferrihk 680 2 565895 NADPH-ferrihk 680 2 565895 NADPH-ferrihk 680 2 710723 NADPH-ferrihk 705 2 710723 nitric-oxide 1147 1 547647 nitric-oxide 1147 1 156575 nitric-oxide	2 S16233 5 G1946 2 S53946 2 T02215 2 T05758 2 A55592 2 A55592 2 A55698 2 T10723 1 A43271 1 156575 1 S3855

## ALIGNMENTS

	RESULT 1 A34286 NADPH-ferrihe N;Contains: N	RESULT 1 A34286 MADPH-ferrihemoprotein reductase (EC 1.6.2.4) - Bacillus megaterium N:Contains: NADPH-ferrihemoprotein reductase (EC 1.6.2.4); unspecific monooxygenase (
	C; Species: Ba C; Date: 10-Se	C;Species: Bacillus megaterium C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
	C, Accession: R; Ruettinger, J. Biol. Chem	AS\$#280; S\$\$555 RTT; Wen, L.P.; Fulco, A.J. L. 264: 10987-10995, 1989
	A; Title: Codi A; Reference r	A;Title: Coding nucleotide, 5' regulatory, and deduced amino acid sequences of P-450-A;Reference number: A34286; MUID:89291834; PMID:2544578
•	A;Accession: A34286 A;Molecule type: DNA A:Residues: 1-1049 <rue></rue>	A34286 Per: DNA 1049 < RUE>
	A; Cross-refer	A; Gross-references: GB:J04832; NID:g142797; PIDN:AAA87602.1; PID:g142798 R:Munro, A.W.: Lindsay, J.G.: Cogdins, J.R.: Relly, S.W.: Price, N.C.
	FEBS Lett. 34	3, 70-74, 1994 fortival and consummingting analysis of the interaction of scolated domains
	A) Reference r	A) Reference number: S43653; MUID:94215710; PMID:8163021
	A; Molecule ty	A, Molecule type: protein
	A; keslaues: 4 C; Genetics:	30-43U;44I-430 <won></won>
	A; Gene: CYP102	Gene: CYP102 Sunerfamily: P450 hifunctional enzyme CYP102. cutochrome P450 homology: flavodoxin
	C; Keywords: C	Keywords: chromoprotein; electron transfer; flavoprotein; FMN; heme; iron; met
	F; 483-1046/Do	262-423/DOMMain: CytConfome P430 nomology <f43> 483-1046/Dommain: NADPH-ferrihemoprotein reductase homology <feh></feh></f43>
	F;401/Binding	F:483-624/Domain: IlaVodoxin nomology <fla> F:401/Binding site: heme iron (Cys) (axial ligand) #status predicted</fla>
	Query Match	***
	Matches 104	best botal similarity 100.0%; Fred. No. 0; Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	Qy 1	1 TIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60
	Db 2	2 TIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 61
	Qy 61	ACDESREDKNLSQALKEVRDFAGDGLFTSWTHEKNWKKAHNILLDSFSQOAMKGYHAMAY 120
	Db 62	
	0y 121	
	pb 122	DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRA 181
	Qy 181	LDEAMNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSDDLLTHMLNG 240
	Db 182	
	Oy 241	KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD 300

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N.Contains: NADPH-ferrihemoprotein reductase (EC 1.6.2.4); unspecific monooxygenase (EC 5.95ecdes: Bacillus subtilis
C;Date: 21-011-2000 #sequence_revision 21-011-2000 #text_change 03-011-2002
C;Accession: A69975
R;Munst, F; Ogaawara, N; Moszer, I; Albertini, A.M; Alloni, G; Azevedo, V; Berter
C; Beron, S; Brouillet, S; Bruschi, C.V.; Caldwell, B; Capuano, V; Carter, N.M.; Chd
A; Ehrlich, S.D; Emmerson, P.T; Entian, K.D; Errington, J; Fabret, C; Ferrari, E.
A; Envolver: Foulger, D; Fritz, C; Fujita, M; Fujita, Y; Fuma, S; Galizzi, A; Galler
iech, J; Harwood, C.R; Henaut, A; Hilbert, H; Holsappel, S; Hosono, S; Hullo, M.F.
A; Authors: Lauber, G; Krogh, S; Kumano, M; Kurita, K; Lapidus, A; Larinois, A; Authors: Lauber, J; Lazarevic, V; Lee, S.M; Levine, A; Liu, H; Masuda, S; Maucel
Y; M; Ogawa, K; Ogiwara, A; Oudega, B; Park, S.H; Parro, V; Pohl, T.M.; Portecelle
Rieger, M; Rivolta, C; Rocha, E; Roche, B; Rose, M; Sadale, Y;; Sato, T.; Scanlon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADV 1020
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                                                           HRDKTIWGDDVEEFRPERFENPSAIPQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKH 420
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akeuchi, M.; Tamakoshi, A.; Tamakoshi, A.; Seknyasha, A.; Seksukasha, A.; Sekeuchi, M.; Tamakoshi, A.; Tasumoto, K.; Yasumoto, M.; 
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Cytochrome P450 / NADPH-cytochrome P450 r homolog yetO - Bacillus subtilis
C;Species: Bacillus Signature
C;Accession: D69799
R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M; Alloni, G; Azevedo, V; Ber C; Brons, S; Broulliet, S; Bruchilet, C.Y; Caldwell, B; Capuano, V; Carter, N.M;
A; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K; Funa, S; Galizzi, A.; Gal
A; Authors: Foulger, D.; Fritz, C.; Fujita, M; Fujita, K; Lapidus, A.; Backowska, A.; Scan, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sakowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tamakoshi, A.; Tamakoshi, A.; Tamakoshi, A.; Tamakoshi, A.; Tamamakoshi, A.; Tamam
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A; Residues: 1-1061 < KUN>
A; Cross-references: GB:299107; GB:AL009126; NID:g2632866; PIDN:CAB12544.1; PID:g26330
A; Cross-references: GB:299107; GB:AL009126; NID:g2632866; PIDN:CAB12544.1; PID:g26330
A; Cross-references: GB:299107; GB:AL009126; NID:g2632866; PIDN:CAB12544.1; PID:g26330
A; Genetics:
C; Genetics:
C; Genetics: C; Genetics: GB:299107; Cytochrome P450 homology; flavodoxin
C; Superfamily: P450 bifunctional enzyme CYP102; cytochrome P450 homology; flavodoxin
C; Keywords: chromoprotein; flavoprotein; heme; iron; metalloprotein
F; 264-425; Comain: cytochrome P450 homology < PEH>
F; 264-425; Comain: cytochrome P450 homology < PEH>
F; 495-632, Chomain: Gytochrome P450 homology < PEH>
F; 495-632, Chomain: Gytochrome P450 homology < PEH>
F; 495-632, Chomain: Gytochrome P450 homology < PEH>
F; 403-1057, Domain: GYtochrome P450 homology < PEH>
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
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100.0%; Pred. No. 1.2e-11;
tive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 28; Conservative
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Best Local Similarity
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us-10-031-146-2.rpr

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NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - Aspergillus niger
N;Alternate names: NADPH-cytochrome P450 oxidoreductase
C;Species: Aspergillus niger
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
C;Accession: S38427
R;Van den Brink, J; van Zeijl, C; van den Hondel, C; van Gorcom, R.
submitted to the EMBL Data Library, October 1993
A;Description: Cloning and characterization of the NADPH cytochrome P450 oxidoreducta
A;Reference number: S38427
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C; Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemo
C; Keywords: flavoprotein; NADP; oxidoreductase
F; 66-691/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F; 66-220/Domain: flavodoxin homology <FLX>
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A;Introns: 45/3; 71/3; 111/2
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemo
C;Keywords: flavoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable NADPH cytochrome reductase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: T37567
R;Wood, V.; Barrell, B.G.; Rajandream, M.A.; Harris, D.; Seeger, K.
R;Wood, V.; Barrell, B.G.; Rajandream, M.A.; Harris, D.; Seeger, K.
A;Reference number: Z21725
A;Reference number: Z21725
A;Reference number: Z21725
A;Reference number: Z21735
A;Reference number: Z31735
A;Reference number: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-693 <VAN>
A;Cross-references: EMBL:Z26938; NID:g408110; PIDN:CAA81550.1; PID:g408111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.4%; Score 15; DB 1; Length 693; 100.0%; Pred. No. 6.8e-06; tive 0; Mismatches 0; Indels
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Pred. No. 0.00052;
0; Mismatches 0;
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Best Local Similarity 100.C
Matches 13; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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C:Species: Schizosaccharomyces pombe
C:Species: 10-Sep-1999 #text_change 03-Jun-2002
C:Accession: S29123; T40324; S20814
R:Wiles: J.S.
Biochem. J. 287, 195-200, 1992
A:Title: Structurally and functionally conserved regions of cytochrome P-450 reductase a saccharomyces pombe CDNA
A:Reference number: S29123; MUID:93038553; PMID:141773
A:Accession: S29123
A:Molecule type: mRNA
A:Reference number: S29123
A:Molecule type: mRNA
A:Reference number: Z1920
A:Reference number: Z1920
A:Reference number: Z21920
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Suberfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemopro
C; Keywords: electron transfer; endoplasmic reticulum; FAD; flavoprotein; FMN; membrane F
F;53-677/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 2
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprd
C;Keywords: flavoprotein
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NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - fission yeast (Schizosaccharomyces pombe
                                                                                   nadph-cytochrome p450 reductase - fission yeast (Schizosaccharomyces pombe) (fragment)
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A; Readidues: 1-678 cwOo>
A; Cross-references: EMBL:AL078627; PIDN:CAB44769.1; GSPDB:GN00067; SPDB:SPBC365.17
A; Experimental source: strain 972h-; cosmid c365
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100.0%; Pred. No. 6.9e-07;
tive 0; Mismatches 0;
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100.0%; Pred. No. 6.7e-07;
tive 0; Mismatches 0;
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Matches 16
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A; Title: Cloning and characterization of the cytochrome P450 oxidoreductase gene from A; Reference number: JC7192; MUID:20145435; PMID:10679206
A; Accession: JC7192
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-710 < YADD>
A; Cross-references: (B:AF195659
C; Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemo C; Keywords: flavoprotein; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - pig
N;Alternate names: NADP-cytochrome P450 reductase
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 04-Dec-1986 #sequence_revision 03-Feb-1994 #text_change 03-Jun-2002
C;Accession: A25584; A00403
E;Handiu, M.; Iyanagi, T.; Miller, P.; Lee, T.D.; Shively, J.E.
Biochemistry 25, 7906-7911, 1986
A;Title: Complete amino acid sequence of NADPH-cytochrome P-450 reductase from porcin A;Reference number: A25584; MUID:87101085; PMID:3099837
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A; Residues: 1-677 < CHAN>
R; Vogel, F.; Lumper, L.
Biochem J. 236, 871-878, 1986
A; Tille: Complete structure of the hydrophilic domain in the porcine NADPH-cytochrome A; Reference number: A00403; MUID:87075664; PMID:3098240
A; Accession: A00403
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A. Residues: 56-162, 'S', 164-173, 'D', 175-338, 'A', 340-377, 'D', 379-399, 'E', 401-445, 'L', 44
A. Residues: 56-162, 'S', 164-173, 'D', 175-338, 'A', 340-377, 'D', 379-399, 'E', 401-445, 'L', 44
C. Superfamily: NaDPH-ferrimenprotein reductase; flavodoxin homology; NaDPH-ferrihemo
C. Keywords: acetylated amino end; electron transfer; endoplasmic reticulum; FAD; flav
F; 76-126/Domain: FAN binding <FRN>
F; 76-126/Domain: NaDPH-ferrihemoprotein reductase homology <FEH>
F; 81-223/Domain: flavodoxin homology <FLX>
F; 451-476/Domain: FAD binding <FRN>
F; 451-476/Domain: experimental
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Pred. No. 0.00065;
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100.0%; Pred. No. 0.006;
iive 0; Mismatches (
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Best Local Similarity 100.(
Matches 13; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
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C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 0.Dec-2000 #sequence_revision 01-Dec-2000 #text_change 03-May-2002
C;Accession: A83726
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler lech, J.; Harwood, C.R.; Henaut, A.; Hibert, H.; Holaspel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapdius, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogdwa, K.; Ogdwa, K.; Oddega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron A; Winters, P.; Wipat, A.; Tamanka, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Tamancho, H.; Yasumoto, K.; Yata, K.; Yata, K.; Yoshida, R.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A; Reference number: A69580; MuID:98044033; PMID:9384377
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-607 <STO>
A;Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB04328.1; GSPDB:GN00
A;Experimental source: strain C-125
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C;Keywords: flavoprotein
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A;Experlmental source: strain 168
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F;68-604/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;70-209/Domain: flavodoxin homology <FLX>
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Best Local Similarity 100.0
Matches 13; Conservative
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A;Molecule type: protein
A;Residues: 2-677 <HANN
A;Note: 551-Gln was also found
R;Yamano, S.; Aoyama, T.; Mcbride, O.W.; Hardwick, J.P.; Gelboin, H.V.; Gonzalez, F.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 31-Dec-1993 #text_change 03-Jun-2002
C;Date: 17-Apr-1993 #sequence_revision 31-Dec-1993 #text_change 03-Jun-2002
C;Accession: A33421; A60557; S21686
R;Haniu, M.; McManus, M.E.; Birkett, D.J.; Lee, T.D.; Shively, J.E.
Biochemistry 28, 8639-8645, 1989
A;Title: Structural and functional analysis of NADPH-cytochrome P-450 reductase from A;Reference number: A33421; MUID:90105390; PMID:2513880
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    Gaps
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rabbit

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A; Molecule type: mRNA
A; Residues: 1-679 < RNIY>
A; Residues: 1-679 < RNIY>
A; Cross-references: GB:X04610; NID:g1543; PIDN:CAA28279.1; PID:g1544
B; Black, S.D.; Coon, M.J.
J. Biol. Chem. 257, 5929-5938, 1982
A; Title: Structural features of liver microsomal NADPH-cytochrome P-450 reductase. Hy
A; Reference number: A05233; MUID:82167456; PMID:6802823
                                                                                                                                                                                                                                      R;Katagirī, M.; Murakami, H.; Yabusaki, Y.; Sugiyama, T.; Okamoto, M.; Yamano, T.; Oh J. Biochem. 100, 945-954, 1986
A;Title: Molecular cloning and sequence analysis of full-length cDNA for rabbit liver A;Reference number: A25505; MUID:87137361; PMID:3029050
                                                                                            C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 03-Jun-2002
C; Accession: A25505; A05233
                                                             NADPH-ferrihemoprotein reductase (EC 1.6.2.4)
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Best Local Similarity 100.
Matches 12; Conservative
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A; Residues: 2-13;45-62 <YA2>
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NAlternate names: NADPH-cytochrome P450 oxidoreductase
C; Species: Cavita porcellus (guinea pig)
C; Date: 03-reb-1994 #sequence_revision 03-reb-1994 #text_change 03-Jun-2002
C; Accession: S27158; S38510
C; Accession: S27158; S38510
C; Accession: S27158; S38510
C; Accession: S27158; S38510
C; Accession: S27158; MUD: 93041995; PMD: 1420354
A; Reference number: S27158; MUD: 93041995; PMD: 1420354
A; Recession: S27158
A; Molecule type: mRNA
A; Reserve mumber: S27158; MUD: 93041995; PMD: 1420354
A; Note: the species identification has been revised in reference S38510
A; Note: the species identification has been revised in reference S38510
B; Objuya, S; Goda, T; Ishizaki, K; Kamataki, T; Shinrike, N.
B; Reference number: S38510; MUD: 93385164; PMID: 8373812
A; Reference number: S38510; MUD: 93385164; PMID: 8373812
A; Contents: annotation; erratum
C; Cinnorfemal: unnotation; erratum
C; Cinnorfemal: unn
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A; Residues: 2-499, 'V, 501-517, 'L', 519-536, 'WH', 539-677 < SHE>
A; Residues: 2-499, 'V, 501-517, 'L', 519-536, 'WH', 539-677 < SHE>
A; Cross-references: GB:S90469; NID:92447306; PIDN:AAB21814.1; PID:9247307
A; Cross-references: GB:S90469; NID:9247306; PIDN:AAB21814.1; PID:9247307
C; Keywords: acetylated amino end; electron transfer; endoplasmic reticulum; FAD; flavopr
F; 1-56/Domain: membrane-bound #status predicted < WEM>
F; 2-677/Product: NADPH-ferrihemoprotein reductase #status experimental < MAT>
F; 80-675/Domain: FMN binding #status predicted < FMN>
F; 80-675/Domain: FMN binding #status predicted < FMN>
F; 84-224/Domain: FAD binding #status predicted < FMD>
F; 84-256/Region: FMN-phosphate binding #status predicted < FAD>
F; 257-326,452-477/Domain: FAD binding #status predicted < FAD>
F; 267-326,452-477/Domain: ABD binding #status predicted < FAD>
F; 267-326,452-477/Domain: ABD binding #status predicted < FAD>
F; 267-326,650-326/Region: FAD-pyrophosphate binding #status predicted < FAD>
F; 266/Binding site: ACETylated amino end (Gly) (in mature form) #status experimental F; 566/Binding site: NADP (Cys) #status experimental
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          DNA cloning, sequence and vaccin
                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-137, 'G',139-577,'DV',580-677 <YAM>
R; Shephard, E.A.; Palmer, C.N.A.; Segall, H.J.; Phillips, I.R.
Arch. Blochem. Biophys. 294, 168-172, 1992
A; Title: Quantification of cytochrome P450 reductase gene expression in human tissues.
A; Reference number: S21686; MUID:92198003; PMID:1550342
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Pred. No. 0.006;
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A;Title: Human NADPH-P450 oxidoreductase: complementary A;Reference number: A60557; MUID:89313720; PMID:2501655 A;Accession: A60557
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                               A; Status: preliminary
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A; Residues: 'PTHDG', 14-39,'NY', 42-52,'N', 54-81 <BLA>
A; Residues: 'PTHDG', 14-39,'NY', 42-52,'N', 54-81 <BLA>
A; Residues: 'PTHDG', 14-39,'NY', 42-52,'N', 54-81 <BLA>
A; Note: the order of the first four residues was not determined
A; Note: the amino end of the mature protein is acetylated
C; Comment: This enzyme, a membrane-bound flavoprotein containing one molecule each of
C; Comment: This enzyme, a membrane-bound flavoprotein reductase; flavodoxin homology; NADPH-ferrihemo
C; Reywords: acetylated amino end; electron transfer; FAD; flavoprotein; FMN; membrane
F; 78-56,Domain: membrane-bound #status predicted <FMN>
F; 78-228/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
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A; Residues: 1-691 A) Corss-references: 1-691 A) Corss-references: 1-691 A) Corss-references: EMBL: U00062; NID: 9488162; PIDN: AAB68904.1; PID: 9488169; GSPDB: GNO R; Yabusaki, Y.; Murakami, H.; Ohkawa, H.
J. Biochem. 103, 1004-1010, 1988
A; Title: Primary structure of Saccharomyces cerevisiae NADPH-cytochrome P450 reductas A; Reference number: A41447; MUID: 89008184; PMID: 3139648
A) Accession: A41447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - yeast (Saccharomyces cerevisiae) N:Alternate names: NADP-cytochrome P450 reductase; protein H8179.8; protein YHR042w C;Species: Saccharomyces cerevisiae C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002 C;Accession: $46735; A41447; B41447
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A;Resdidues: 1-422,'N',424-473,'G',475-691 <YAB>
A;Cross-references: GB:D13788; GB:D00316; NID:g218452; PIDN:BAA02936.1; PID:g218453
A;Accession: B41447
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F:88-96/Regolon: FMN-Phosphate binding #status predicted
F:268-327,453-478/Domain: FAD binding #status predicted <FAD>
F:294-297/Region: FAD-pyrophosphate binding #status predicted
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Live 0; Mismatches 0; Indels
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A; Description: The sequence of S. cerevisiae cosmid 8179.
A; Reference number: $46732
A; Accession: $46735
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A;Cross-references: MIPS:YHR042w; SGD:S0001084
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C; Function:

A; Description: electron transfer; oxidoreductase C; Superfamily: NADPH-ferrihemopro C; Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein C; Keywords: electron transfer; endoplasmic reticulum; flavoprotein; NADP; oxidoreductase F; 61-690, Domain: NADPH-ferrihemoprotein reductase homology <FEH> 0; Gaps Ouery Match 1.1%; Score 12; DB 1; Length 691; Best Local Similarity 100.0%; Pred. No. 0.0061; Matches 12; Conservative 0; Mismatches 0; Indels g ò

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Search completed: May 29, 2003, 08:44:50 Job time : 50 secs

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US-10-031-146-2 1048 1 TIKEMPQPKTFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048 112892 segs, 41476328 residues OLIGO Gapop 60.0 , Gapext 60.0 Perfect score: Scoring table: Searched: Sequence:

Total number of hits satisfying chosen parameters: 0 Word size :

112892

Post-processing: Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P14779 bacillus me		008394 bacillus su	P36587 schizosacch	P16435 homo sapien	cavi	P37040 mus musculu		P00389 oryctolagus		P37116 phaseolus a	Q09744 schizosacch	P19618 salmo trutt	Q9z0j4 mus musculu	P29476 rattus norv		_		-		O19114 oryctolagus	_		_		-		Q06518 rattus norv		054705 cavia porce	6	コ	P79152 capra aegag
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[1]
MEDLINE=89291834; PubMed=2544578;
MEDLINE=89291834; PubMed=2544578;
Ruettinger, R.T., Wen L.-P., Fulco A.J.;
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"Coding nucleotide, 5' regulatory, and deduced amino acid sequences
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MEDLINE=99162523; PubMed=10051560;
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                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
        Biochemistry 40:13456-13465(2001).
-!- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXGENASE. CATALYSES HYDROXYLATION OF MEDIUM AND LONG-CHAIN FATTY ACIDS AT OMEGA-1, OMEGA-2 AND OMEGA-3 POSILIONS, WITH OPTIMUM CHAIN LENGTHS OF 14-16 CARBONS (LAURIC, MXRISTIC, AND PALMITIC ACIDS). THE REDUCTASE DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
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R InterPro; IPR001309; FAD_binding.
R InterPro; IPR001309; FAD_binding.
R InterPro; IPR001309; FAD_binding.
R InterPro; IPR001431; Oxred_FAD/NAD(P).
Pfam; PF000175; NAD_binding; 1.
R Pfam; PF00057; FAD_binding; 1.
R Pfam; PF00057; FAD_binding; 1.
R Pfam; PF00057; FAD_binding; 1.
R PRINTS; PF00031; FPNCR.
R PRINTS; PF00086; CYTOCHROME_P450; 1.
R PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                             oxidized flavoprotein + H(2)0.
COGACTOR: FAD AND FMN.
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
P450 FAMILY.
                                                                                          CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
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CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH
 role of water in the mechanism of P450BM-3.";
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16-OCT-2001 (Rel. 40, Last sequence update)
16-UN-2002 (Rel. 41, Last annotation update)
Probable bifunctional P-450:NADPH-P450 reductase 2 [Includes:
Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase
(EE 1.6.2.4)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J., Duesterhoeft A., Ehrlich S.D.; "Sequence of the Bacillus subtilis genome region in the vicinity of the lev operon reveals two new extracytoplasmic function RNA polymerase signa factors Sigv and Sigz."; Microbiology 143:2939-2943(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1054 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOVSEADARLWLQQLEEKGRYAKDVWAG 1048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98044033; PubMed=9384377;
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008336;
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RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Deniel R.A., Denizot F., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., RA Guiseppi G., Guy B.J., Haga K., Hatech J., Hawood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., RA Kobayashi Y., Koetter P., Koningstein G., Kroph S., Kumano M., Kobayashi Y., Levine A., Liu H., Masuda S., Mauel C., Medique C., RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Kumano M., None D., O'Rellly M., Ogawa K., Oqiwara A., Oudega B., Park S.H., RA Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Rayolta C., Rocha E., Roche B., Rose M., Sadaie Y., Rakeyori J., Scanlan E., Schleich S., Schroeter R., Scoffone F., Setjuchi J., Skowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Rakeuchi M., Tamakoshi A., Tanaka T., Takahashi H., Takemaru K., Varaconi E., Waller R., Wedler H., Weitzenegger T., Wambutt R., Wedler H., Weitzenegger T., Windler S., Windler E., Wedler H., Weitzenegger T., The complete genome sequence of the Gram-positive bacterium Bacillus F. Fubilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ferrocytochrome.
-!--CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
cxidized flavoprotein + H(2)0.
-!--CORACTOR: RD AND FMN (By similarity).
-!-- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME P450 (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Electron transport; Membrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U93874; AAB80867.1; -
R EMBL; U93874; CAB14658.1; -
R HSSP; PI4779; 1JPE.
R Subtilist; BG12299; CypE.
R InterPro; IPR001128; Cytochrome_P450.
R InterPro; IPR001128; EPN_Cyt_redctse.
R InterPro; IPR001226; Flavodoxin.
R InterPro; IPR00125; Flavodoxin.
R Pfam; PF00067; P450; 1.
R Pfam; PF00058; flavodoxin; 1.
R Pfam; PF00658; flavodoxin; 1.
R Pfam; PF00658; Fav_Dinding; 1.
R Pfam; PF00667; Fav_Dinding; 1.
R PRINTS; PR00371; FPNCR.
R PRINTS; PR00385; P450.
R PRINTS; PR00385; P450.
R PRINTS; PR0086; CTYCCHROME_P450; 1.
R Oxidoreductase; Monooxygenase; Electron transport; Membre Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEME (BY SIMILARITY).
W; 705F8E27866CA110 CRC64;
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1054 AA; 118675 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 390:249-256(1997)
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Length 1054;

DB 1;

2.7%; Score 28;

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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
A Chalsar H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Mulbert H., Holsappel S., Hosono S., Lauber J., Garadi G.,
RA Kobayashi Y., Kootter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita R., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kobayashi Y., Koottere P., Mizuno M., Moestl D., Nekai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Saklguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Takeuchi M., Tamakoshi A., Taragal T., Tarkahashi H., Takemari R.,
RA Takeuchi M., Tamakoshi A., Taragaler E., Wedler R., Weitzenegger T.,
RA Winters P., Wabbat A., Yamamoto H., Vamane K., Yasumoto K., Yata K.,
RA Winters P., Wabbat A., Yamamoto H., Vamane K., Yasumoto K., Yata K.,
R. Toshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Danchin A.,
R. Pipt Complete genome sequence of the Gram-positive bacterium Bacillus
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                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable bifunctional P-450:NADPH-P450 reductase 1 [Includes:
CYtochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase (EC 1.6.2.4)].
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97453479; PubMed-9308178; Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J., Bototin A., Purnelle B., Hilbert H., Lauber J., Duesterhoeft A., Ehrlich S.D.; "Sequence of the Bacillus subtilis genome region in the vicinity of the lev operon reveals two new extracytoplasmic function RNA polymerase sigma factors Sigv and Sig2."; Microbiology 143:2939-2943(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ferrocytochrome.
-!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
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                Indels
                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. NCBI_TaxID=1423;
                ö
100.0%; Pred. No. 9.3e-20;
                                                                                                                                                      1061 AA.
                0; Mismatches
                                                           252 LDDENIRYQIITFLIAGHETTSGLLSFA 279
                                           249 LDDENIRYQIITFLIAGHETTSGLLSFA 276
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           28; Conservative
                                                                                                                                                        STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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           Matches
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                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
-1- COFACTOR: FAD AND FWN (By similarity).
-1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme; Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP; Complete proteome.
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01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
NADPH-Cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              475 1061 NADPH-P-450 REDUCTASE.
403 403 HEME (BY SIMILARITY).
1061 AA; 119467 MW; 7915DACC20578978 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Lens.
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100.0%; Pred. No. 1.1
                                                                                                                                                                                                                                                                                                                                                                                     Subtilist; BG12871; cypb.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR003097; FAD_binding.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001226; Flavodoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pfam; pro0067; p450; 1.
Pfam; pr00067; NAD_binding; 1.
Pfam; Pr00158; flavodoxin; 1.
Pfam; Pr00667; FAD_binding; 1.
PRINTS; PR00371; PPNCR.
PRINTS; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001433; Oxred_FAD/NAD(P)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 DMTRLTLDTIGLCGFNYRFNS 164
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MEDLINE=21848401; PubMed=11859360;
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                                                                                                                                                                                                                                                                                                          EMBL; D87979; BAA20123.1; -. EMBL; Z99107; CAB12544.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                     P450 FAMILY.
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RA Sgource J., Peat N., Rajandream M.A., Lyne M., Lyne R., Stewart A., RA Sgource J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Shollingworth T., Churcher C.M., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Gentles S., Goble A., Haminn N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., Andrex K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA Moodey P., Mungall K., Murphy L., Niblett D., Odell C., Collyver K., O'Neil S., Mungall K., Murphy L., Niblett D., Odell C., Ra Ratherford K., Rutter S., Squares R., Squares S., Stevens K., Stevens K., Stanpokar G., Yolckeart G., Aert R., Robben J., Grynonprez B., RA Taylor R., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Weltjens I., Vonstreels E., Rieger M., Schaefer M., Meiler-Huer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Raber M., Cabager M., Schaefer M., Meiler S., Ra Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Reinhardt R., Pohl T.M., RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., RA Daga R.R., Cruzado L., Jimene Z., Banktony J., Forsburg S.L., Ra Spakovski G.V., Ussery D., Barrell B.G., Nurse P., Ra Shakovski G.V., Ussery D., Barrell B.G., Nurse P., R. The genome sequence of Schlzosaccharomyces pombe.";

"The genome sequence of Schlzosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
SIMILARITY: THE FMN-SINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOWOLOGUS WITH FERREDXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
6AEDDFBAGDE39C8F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00175; NAD_binding; 1.
Pfam; PF00258; flavodoxin; 1.
Pfam; PF00667; FAD_binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL078627; CAB44769.1; -.
EMBL; AL034463; CAA22429.2; -.
PIR; S29123; S29123.
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HSSP; P00388; 1AMO.
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Gaps

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1.5%; Score 16; DB 1; Length 678; 100.0%; Pred. No. 1.1e-07; ive 0; Mismatches 0; Indels

Conservative

Local Similarity nes 16; Conserv

Best Loca Matches

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murakami H.O., Ogawa H., Nisimoto Y.; "cDNA closhing and characterization of NADPH-cytochrome P-450 reductase in human HL-60 cell."; Eubmitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92198003; PubMed-1550342;
Shephard E.A., Palmer C.N., Segall H.J., Phillips I.R.;
"Quantification of cytochrome P450 reductase gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
-i- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                       Haniu M., McManus M.E., Birkett D.J., Lee T.D., Shively J.E.; "Structural and functional analysis of NADPH-cytochrome P-450 reductase from human liver: complete sequence of human enzyme and NADPH-binding sites."
                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
                                                                                                                    P16435; Q16455; Q9H3M8; 01-AUG-1990 (Rel. 15, Created) 01-AUG-1990 (Rel. 15, Created) 01-AUG-1990 (Rel. 15, Last sequence update) 15-UNN-2000 (Rel. 41, Last annotation update) NADPH-Cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Czerwinski M., Sahni M., Madan A., Parkinson A.;
"Polymorphism of human CYPOR: expression of new allele.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arch. Biochem. Biophys. 294:168-172(1992).
                                                                                                                                                                                                                                                                                                                                                    MEDLINE-90105390; PubMed=2513880;
                                                                                                                                                                                                                                                                                                                                                                                                                         NADPH-binding sites.";
Biochemistry 28:8639-8645(1989).
                   534 IMVGPGTGVAPFRGEV 549
899 IMVGPGTGVAPFRGFV 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- COFACTOR: FAD AND FMN.
                                                                                                                                                                                                                                     Homo sapiens (Human)
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NCPR_MOUSE
P37040;
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MOD_RES
NP_BIND
NP_BIND
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                            Endoplasmic reticulum;
                                                                                                                                                                                                                      ACETYLATION.
FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Obdiya S., Goda T., Ishizaki K., Kamataki T., Shinriki N.; "Molecular cloning and sequence analysis of guinea-pig NADPH-cytochrome P-450 oxidoreductase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
1-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
                                                                                                                                                                                                                                                                                                                                                                   core 12; DB 1; Length 676; Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Obgiya S., Goda T., Ishizaki K., Kamataki T., Shinriki N.;
Biochim. Biophys. Acta 1174:313-313(1993).
                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                     M -> L (IN REF. 4).
F -> L (IN REF. 2 AND 4).
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883EA13797020D70 CRC64;
                                                                                                                                                                                           Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endc
Membrane; Acetylation; Polymorphism; 3D-structure.
                                                                                                                                                                                                                                                                                       /FTId=VAR_004617.
R -> Q.
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                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. ...
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                                                                                           InterPro; IPR003097; FAD_binding.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001094; Flavddxin_like.
InterPro; IPR0011226; Flavddxin.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00567; FAD_binding; 1.
         send an email to license@isb-sib.ch)
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MEDLINE-93041995; PubMed-1420354;
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                                    EMBL; AF258341; AAG09798.1; -. EMBL; AA051763; BAB18572.1; -. PIR; A33421; A33421. PDB; IBIC; 24-NOV-99.
                                                                                                                                                                                                                                                                                                                                                  76558 MW;
                           EMBL; S90469; AAB21814.1; -.
                                                                                                                                                                        PRINTS; PR00369; FLAVODOXÍN.
PRINTS; PR00371; FPNCR.
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         899 IMVGPGTGVAPF 910
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517
536
676 AA;
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0
-i- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                     -!- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO ORIGINATE FROM MOUSE.
                                                                                                                                                                -i- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
-i- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
ACCTULATION (BY SIMILARITY).
FWN (PYRINDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
                           CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAD (FLAVIN PÁRT) (BY SIMILARÍTY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
                                                                                    NADP(+) + 2
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01-JUN-1994 (Rel. 29, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 12; DB 1; Length 677; Pred. No. 0.0013; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4CA758F28EB84938 CRC64;
                                                      TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 677 AA.
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HSSP: P00388; Jawo.
InterPro; IPR003097; FAD_binding.
InterPro; IPR001094; FPA_cyt_redctse.
InterPro; IPR001094; FPAdoXin_like.
InterPro; IPR001265; Plavdoxin_like.
InterPro; IPR001226; Plavdoxin_like.
Fam; PF00175; NAD_binding; 1.
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00558; flavddoxin; 1.
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MEDLINE=94281246; Pubmed=8011664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D10498; BAA01385.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.18;
                                                                                                                                              -1 - COFACTOR: FAD AND FMN.
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324
460
547
640
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                                                                                                                  ferrocytochrome.
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450 4
529 5
624 6
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tes 12; Conserv
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                                                                                                                                                                                                                                                                                                                             REDUCTASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ő
                   functional expression in yeast.";
Blochim. Biophys. Acta 1186:137-141(1994).
-!- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
- FOUCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM INTCROSOMES. IT CAN ALSO PROVIDE ELECTRON
TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
-!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
"Mouse NADPH-cytochrome P-450 oxidoreductase: molecular cloning and
                                                                                                                                                                              SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACETYLATION (BY SIMILARITY).
FEMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
NOGSC144D0E1G5EF8 CRC64;
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Sus.
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16-OCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 12; DB 1; Length 677;
Pred. No. 0.0013;
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Cetartiodactyla, Suina, Suidae,
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Mismatches
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InterPro; IPR001099; FPN_cyt_redctse.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001226; Flavdoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00175; NAD_binding; 1.
Pf00258; flavodoxin; 1.
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D17571; BAA04496.1; -.
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                                                                                                                                                               -1- COFACTOR: FAD AND FMN.
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528 IMVGPGTGVAPF 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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450
529
624
677 AA;
                                                                                                                                                ferrocytochrome
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P04175;
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NP_BIND
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Matches
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELECTRON TRANSFER FROM NADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                          MEDINE-87075664; PubMed-3098240;
Vogel F., Lumper L.;
"Complete structure of the hydrophilic domain in the porcine NADPH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
-1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
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FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. J. 236:871-878(1986).
-1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NATO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
   .
E
                                                                                                                                                                                       Haniu M., Iyanagi T., Miller P., Lee T.D., Shively J.E.;
Complete amino acid sequence of NADPH-cytochrome P-450 reductase
from porcine hepatic microsomes";
Biochemistry 25:7906-7911(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2 ferrocytochrome.
Amborn J., Preiss B., Stender B., Viale M., Repp R.Z., Lampert Stroger M., Lumper L.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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T -> A (IN REF. 3).

D -> D (IN REF. 3).

-> E (IN REF. 3).

R -> L (IN REF. 3).

N -> D (IN REF. 2).

V -> L (IN REF. 2).

V -> L (IN REF. 2).

V -> L (IN REF. 3).

Z -> N (IN REF. 3).

Z -> N (IN REF. 3).
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NADP (ADP PART) (BY
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InterPro; IPR0013097; FAD binding.
InterPro; IPR0013097; FPAD binding.
InterPro; IPR001094; FPAU-cyt_redctse.
InterPro; IPR00126; Flavodoxin_like.
InterPro; IPR00126; Flavodoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00258; flavodoxin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytochrome P-450 reductase.
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PIR; A25584; A25584.
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677 AA;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 56-677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T. Biol. Chem. 257:5929-5938(1982).

1- BIOL. CHEM. 257:5929-5938(1982).

1- CUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME PASO IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.

1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE EN MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
SIMILARITY: THE FWN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOWOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBL_raxID-9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Black S.D., Coon M.J.;
"Structural features of liver microsomal NADPH-cytochrome P-450
reductase. Hydrophobic domain, hydrophilic domain, and connecting
                                                                                                                                                                                                                                                                                                                                                                                                                                   Katagiri M., Murakami H., Yabusaki Y., Sugiyama T., Okamoto M., Yamano T., Ohkawa H.; Molecular clonding and sequence analysis of full-length cDNA for rabbit liver NADPH-cytochrome P-450 reductase mRNA."; J. Biochem. 100:945-954(1986).
                                    ö
                                                                                                                                                                                                P00389;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
Score 12; DB 1; Length 677;
                                  0; Indels
               100.0%; Pred. No. 0.0013; ive 0; Mismatches 0
                                                                                                                                                                                     679 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003097; FAD_binding.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001226; Flavdoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P)
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00258; flavodoxin; 1.
                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Liver;
MEDLINE-87137361; PubMed-3029050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Liver;
MEDLINE=82167456; PubMed=6802823;
                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D00101; BAA00063.1; -. ERML; X04610; CAA28279.1; -. PIR; A25505; A25505. PIR; A05233; A05233.
                                                                  899 IMVGPGTGVAPF 910
                                                                                     COFACTOR: FAD AND FMN.
                                 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARTIAL SEQUENCE OF 1-81.
                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P16435; 1B1C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REDUCTASE.
                                                                                                                                                                                    NCPR_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region.";
Query Match
                   Best Local
                                                                                                                                                    RESULT 9
NCPR_RABIT
                               Matches
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STRAIN-S288C / AB972;
MEDLINE-94378003; PubMed-8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latrellle P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 1-12 AND 44-61.
MEDLINE-89008184; PubMed-3139648;
Yabusaki Y., Murakami H., Ohkawa H.;
"Primary structure of Saccharomyces cerevisiae NADPH-cytochrome P450 reductase deduced from nucleotide sequence of its cloned gene.";
J. Biochem. 103:1004-1010(1988).
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                       Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
                                                                                                             FWN (PYRIMIDINE PART) ("LEATTY).
FAD (APP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
YW -> NY (IN REF. 2).
E -> N (IN REF. 2).
                                                                                                                   (PYRIMIDINE PART) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 265:2077-2082(1994).

-1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NATION TYOLOGHNOMED P450 IN MAICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.

-1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
-i- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGGUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE REDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1990 (Rel. 15, Created)
01-FBB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADPH-Cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
NCPI OR NCPRI OR PRDI OR YHR043W.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                            DB 1; Length 679;
0.0013;
hes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetales; Saccharomycetaceae; Saccharomyces NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              690 AA.
                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                Score 12;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
PF00667; FAD_binding; 1.
                                                                                                                                                                                                                                      53 I
                                                                                                                                                                                                                                                                                                1.18; 8
            PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- COFACTOR: FAD AND FMN.
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                                                                                                                                                                                                                                                                                                                                                                                                530 IMVGPGTGVAPF 541
                                                                                                                                                                                                                                                                                              Query Match 1.1
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                            Membrane; Acetylation.
                                                                                                                                                                                                               40
53
679 AA;
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CONFLICT
SEQUENCE
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NP_BIND
NP_BIND
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NCPR_YEAST
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01-0cr-1994 (Rel. 30, Last sequence update)
16-0cr-2001 (Rel. 40, Last annotation update)
16-0cr-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
Phaseolus aureus (Mung bean) (Vigna radiata).
Enkaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP-PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- COFACTÓR: FAD AND FMN.
--!- SUBACELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE
ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
-!- PTM: GLYCOSYLATED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 12; DB 1; Length 690;
Pred. No. 0.0013;
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-> N (IN REF. 1).
FEFA18F6AB2BBDF5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. No. 0.0 cive 0; Mismatches
                                                                                                                                                                                                   SGD; SGO01084; NCP1.
InterPro; IPR0013097; FAD_binding.
InterPro; IPR0013097; FPD_cyt_redctse.
InterPro; IPR001094; Flavodoxin_like.
InterPro; IPR001226; Flavodoxin.
InterPro; IPR001433; Oxred_FRD/NAD(P).
Pfan; PF00175; NAD_binding; 1.
Pfan; PF00258; flavodoxin; 1.
Pfan; PF00567; FAD_binding; 1.
PR.NTS; PR00366; FLAVODOXIN.
                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76640 MW;
                                                                                                            EMBL; D13788; BAA02936.1; -. EMBL; U00062; AAB68904.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.1%;
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179
311
445
554
654
                                                                                                                                                  PIR; A41447; A41447.
PIR; S46735; S46735.
HSSP; P00388; IAMO.
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422 4
690 AA;
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P37116;
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NP_BIND
NP_BIND
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NP_BIND
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NCPR_PHAAU
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FAD (ADP PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
M-LINKED (GLCNAC. . . ) (POTENTIAL).
M-LINKED (GLCNAC. . . ) (POTENTIAL).
M, 592966167E8561DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001909; FAD_binding.
InterPro; IPR001709; FAD_binding.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR0011094; Flavdoxin_like.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00258; Flavdoxin; 1.
Pfam; PF00567; FAD_binding; 1.
PRINTS; PR00371; FPNCN.
Oxidoreductase; Flavoprotein; FAD; NADP; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, AND GLUTATHIONE REDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      571 AA
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MEDLINE-21848401; PubMed-11859360;
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475
562 Ni
254
339
76506 MW
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639
275
339
690 AA;
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NCBI_TaxID=4896;
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Matches 11; Conserv
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YB63_SCHPO
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Membrane.
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NON_CONS
SEQUENCE
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  HID DESCRIPTION OF THE PROPERTY OF THE PROPERT
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               Woodward J., Volckaert G., Aerr R., Robben J., Grymonprez B.,
Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Gabel C., Puchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
B Drzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
R Gar P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Goffeau A., Cadleu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Dominguez A., Revuelta J.L., Moreno S., Amistrong J., Forsburg S.L.,
Cerrutti L., Lowe T., Mocmoo S., Amistrong J., Forsburg S.L.,
R Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
"The genome sequence of Schizosaccharomyces pombe.";
"In Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Structural comparison between the trout and mammalian hydrophilic
"Structural comparison between the trout and mammalian hydrophilic
domain of NADPH-cytochrome P-450 reductase.";
J. Chromatogir A 397:123-136(1987).
-1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
-1- CATALYTIC ACTIVITY: NADPH + 2 ferilcytochrome = NADP(+) + 2
  Walsh S.V., Warren T., Whitehead S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COFACTOR: FAD AND FMN.
SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmo trutta (Brown trout).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Oxidoreductase; Flavoprotein; FAD.
SEQUENCE 571 AA; 63976 MW; D2EE992789307249 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 10; DB 1; Length 571;
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1991 (Rel. 17, Created)
1-FEB-1991 (Rel. 17, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
NCBL_TaxID-8032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              601 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z54140; CAA90816.1; -.
InterPro; IPR003097; FAD_binding.
InterPro; IPR001433; Oxred_FAD/NAD(P).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
Taylor K., Taylor R.G., Tivey A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-88008061; PubMed-3116019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00175; NAD_binding; 1. Pfam; PF00667; FAD_binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        906 GVAPFRGFVQ 915
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P19618;
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Dev. Neurosci. 19:224-231(1997).

-i- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN THE BRAIN AND PERIPHERAL NERVOUS SYSTEM, NO DISPLAYS MANY PROPERTIES OF A NEUROTRANSMITTER. ISOFORM NNOS MU MAY BE AN EFFECTOR ENZYME FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DILLIC OXIGE + N NADP(+).

COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TERAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF THE ENZYME (BY SIMILARITY).

THE ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN. INHIBITED BY N-NOS-INHIBITING PROTEIN (PIN) WHICH MAY PREVENT THE DIMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOSI_MOUSE STANDARD; PRT; 1429 AA.
0920J4; 064208;
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 40, Last annotation update)
Nitric-oxide synthase, brain (EC 1.14.13.39) (NOS, type I) (Neuronal NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE-93312283; PubMed-7686743; Ogura T., Yokoyama T., Fujisawa H., Kurashima Y., Esumi H.; Structural diversity of neuronal oxide synthase mRNA in the nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Skeletal muscle;
MEDIINE-96212184; PubMed-8626668;
Silvagno F., Xia H., Bredt D.S.;
"Neuronal nitric-oxide synthase-mu, an alternatively spliced isoform expressed in differentiated skeletal muscle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THE DYSTROPHIN COMPLEX.
                                                                                                                                                InterPro; IPR001094; Flavdóxin_like.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97351924; PubMed-9208206;
Brenman J.E., Xia H., Chao D.S., Black S.M., Bredt D.S.;
"Regulation of neuronal nitric oxide synthase through alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE SPLICING (ISOFORMS NNOS BETA; NNOS GAMMA AND NNOS MU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                       68304 MW; BC801767DE1D44C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 193:1014-1022(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS N-NOS-1 AND N-NOS-2). STRAIN-BALB/C; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.0%; Score 10; DB
100.0%; Pred. No. 0.1
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 271:11204-11208(1996).
                                                                                        HSSP; P16435; 1B1C.
InterPro; IPR001709; FPN_cyt_redctse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM NNOS MU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                              427
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                                                                                                                                                                                                                                                                                                                                  426
434
434
601 AA;
                                                    PIR; A28577; A28577
HSSP; P16435; 1B1C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-10090;
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10;
                                SEQUENCE
    VARSPLIC
                                                                                            Matches
                                                                                                                                                                                                RESULT 15
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                                                                                                                                                                                                               NOS1_RAT
                                                                                                                                                                                                                             g
         -1- SUBURIT: HOMODIMER (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: IN SKELETAL MUSCLE, NNOS IS LOCALIZED BENEATH THE SARCOLEMAA OF PAST-TWITCH MUSCLE FIBER BY ASSOCIATING WITH THE DYSTROPHIN GLYCOPROTEIN COMPLEX.
-1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; N-NOS-1 (SHOWN HERE), N-NOS-2, NNOS BETA, NNOS GAMAM AND NNOS MU/MUSCLE-SPECIFIC; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN THE NERVOUS SYSTEM: EXPRESSED IN CEREBRUM, OLFACTORY BUILD, HIPPOCAMPUS, MIDBRAIN, CEREBELLUM, PONS, MEDLIAA OBLONGATA, AND SPINAL CORD. ALSO FOUND IN SKELETAL MUSCLE, FIBERS, AND IN SPLEN, HERRY TY REGULATED.
IN SKELETAL MUSCLE, FIBERS, AND IN SPLEN, HERRY TY REGULATED.
IN SKELETAL MUSCLE, FIBERS, AND IN SPLEN, HERRY TY REGULATED.
IN SKELETAL MUSCLE, FIBERS, AND IN SPLEN, HERRY TY REGULATED.
IN STATEM, NNOS BETA AND GAMMA OCCUR IN A REGION-SPECIFIC MANNER IN THE BRAIN AND NNOS BETA EXPRESSION IS DEVELOPMENTALLY REGULATED.
INNOS MU IS ONLY FOUND IN MATURE SKELETAL AND CARDIAC MUSCLES.
-1- DOMAIN: THE DIS DOMAIN IN THE N-TERMINAL PART OF THE NEURONAL ISOFORM PARTICIPATES IN PROTEIN-PROTEIN INTERACTION, AND IS RESPONSIBLE FOR TARGETING NNOS TO SYMAPTIC MEMBRANES IN MUSCLES.
-1- DOMAIN: THE DIS DOMAIN IN THE N-TERMINAL PART OF THE NEURON AND IS RESPONSIBLE FOR TARGETING NNOS TO SYMAPTIC MEMBRANES IN MUSCLES.
-1- DISEASE: IN MOX MICE (MOUSE MODEL OF DYSTROPHINOPATHY) THE DYSTROPHIN COMPLEX IS DISRUPTED AND NNOS IS DISPLACED FROM SARCOLEMMA AND ACCUMULATES IN THE CYTOSOL.
-1- SIMILARITY: BELONGS TO THE NOS FAMILY.
-1- SIMILARITY: CONTAINS I PDE/PHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@license.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEME (BY SIMILARITY).
CALMODULIN-BINDING (POTENTIAL).
FAD (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FIAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
MADF (ADP PART) (BY SIMILARITY).
MISSING (IN ISOFORM NNOS BETA).
MISSING (IN ISOFORM NNOS GAMMA).
MISSING (IN ISOFORM NNOS GAMMA).
MISSING (IN ISOFORM NNOS CAMMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNOS-INHIBITING PROTEIN (PIN)-BINDING (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oxidoreductase; NADP; FAD; FWN; Calmodulin-binding; Heme; Alternative splicing; Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004030; NO_synthase.
InterPro; IPR001433; Oxred_FAD/NAD(P).
InterPro; IPR001478; PDZ.
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00258; flavodoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003097; FAD_binding.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001094; Flavdoxin_like.
THE PROTEIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001226; Flavodoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00667; FAD_binding; 1. Pfam; PF02898; NO_synthase; 1. PRINES; PR00369; FLAVODOXIN. PRINTS; PR00371; FP078. SWART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D14552; BAA03415.1; -. EMBL; S81982; AAB36469.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS60001; NOS; 1
PROSITE; PS50106; PDZ; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00595; PDZ; 1
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VARSPLIC
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NP_BIND
NP_BIND
NP_BIND
NP_BIND
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oxidoreductase.";
J. Biol. Chem. 276:37506-37513(2001).
J. Biol. Chem. 276:37506-37513(2001).
HIP DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN THE BRAIN AND
PERIPHERAL NERVOUS SYSTEM, NO DISPLAYS MANY PROPERTIES OF A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.25 ANGSTROMS) OF 14-125.
MEDLINE-99238815; Pubmed=10221915;
Hillier B.J., Christopherson K.S., Prehoda K.E., Bredt D.S., Lim W.A.;
"Unexpected modes of PDZ domain scaffolding revealed by structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM PNNOS).
STRAIN=Fischer 344; TISSUE-Penis;
MEDLINE-96400219; Pubmed-8806605;
MAGGE T., Fuentes A.M., Garban H., Rajavashisth T., Marquez D.,
Rodriguez J.A., Rajfer J., Gonzalez-Cadavid N.F.;
"Cloning of a novel neuronal nitric oxide synthase expressed in penis
839 839 K -> KYPEPLRFFPRKGPSLSHVDSEAHSLVAARDSOHR (IN ISOFORM NNOS MU).
1429 AA; 160472 MW; 3782848D65B41BFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOS1_RAT STANDARD; PRT; 1429 AA.
P29476; P70594;
01-APR-1993 (Rel. 25, Carated)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nitric-oxide synthase, brain (EC 1.14.13.39) (NOS, type I) (Neuronal NOS) (N-NOS) (NNOS) (Constitutive NOS) (NC-NOS) (BNOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) - citrulline +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloned and expressed nitric oxide synthase structurally resembles
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Sato Y., Sagami I., Matsui T., Shimizu T.;
"Unusual role of Tyr588 of neuronal nitric oxide synthase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang J., Martasek P., Paschke R., Shea T., Masters B.S.S.,
Kim J.-J.P.;
                                                                                                                        Length 1429;
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Biochem. Biophys. Res. Commun. 281:621-626(2001).
                                                                                                                                                                                               Indels
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                                                                                                                            Score 10; DB 1;
Pred. No. 0.27;
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100.0%; Pre-
0; }
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytochrome P-450 reductase.";
Nature 351:714-718(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and lower urinary tract.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nNOS-syntrophin complex.";
Science 284:812-815(1999).
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                             1172 PRYYSISSSP 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
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                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Snyder S.H.;
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                                                            THE ENZYME (BY SIMILARITY)

-I- ENZYME (BY SIMILARITY)

-I- ENZYME (BY SIMILARITY)

N-NOS-INHIBITING PROTEIN (PIN) WHICH MAY PREVENT THE DIMERIZATION OF THE PROTEIN (PIN) WHICH MAY PREVENT THE DIMERIZATION OF THE PROTEIN (PIN) WHICH MAY PREVENT THE DIMERIZATION OF THE PROTEIN (BY SIMILARITY).

-I- SUBGUILT: HOMODIMER (BY SIMILARITY).

-I- SUBGELLULAR LOCATION: IN SKELETAL MUSCLE, NNOS IS LOCALIZED BENEATH THE SARCOLEMMA OF FAST-TWAITCH MUSCLE FIBER BY ASSOCIATING WITH THE DYSTROPHIN GLYCOPROTEIN COMPLEX (BY SIMILARITY).

-I- ALTERNATIVE PRODUCTS: 3 ISOFORMS; N-NOS-1 (SHOWN HERE), N-NOS-2 AND PNNOS; ARE PRODUCED BY ALTERNATIVE SPLICING.

-I- TISSUE SPECIFICITY: ISOFORM N-NOS1 IS EXPRESSED IN BRAIN. ISOFORM PNNOS; BADDER AND LIVER, AND IS EXPRESSED IN THE PELLAR NNOS IN THE PELLOL.

MUSCLE, AND COEXISTS WITH THE CEREBELLAR NNOS IN THE PELVIC MUSCLE, AND SARLETAL NUSCLE, AND SARLETAL NUSCLES 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).

HEME (BY SIMILARITY).

CARACODULIN-BINDING (POTENTIAL).

FAN (PYRIMIDINE PART) (BY SIMILARITY).

FAD (FLAVIN PART) (BY SIMILARITY).

NADP (RIBOSE PART) (BY SIMILARITY).

NADP (ADP PART) (BY SIMILARITY).

NADP (ADP PART) (BY SIMILARITY).

NADP (ADP PART) (BY SIMILARITY).

MISSING (IN ISOPORM N-NOS-2).

K -> KYPPELRFFPRKGPSLSHVDSEAHSLVAARDSQHR (IN ISOFORM PNNOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNOS-INHIBITING PROTEIN (PIN)-BINDING (BY
                      COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FWN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50% DECREASE OF ACTIVITY 30% DECREASE OF ACTIVITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE NOS FAMILY.-!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
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InterPro; IRR003097; FAD_binding.
InterPro; IRR001094; Flavdoxin_like.
InterPro; IRR001226; Flavdoxin.
InterPro; IRR004030; NO_synthase.
InterPro; IRR004030; NO_synthase.
InterPro; IRR001433; Oxred_RAD/NAD(P).
InterPro; IRR001478; PDZ.
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Y->S:
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nitric oxide + N NADP(+)
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PDB; 1QAV; 06-MAR-00.
PDB; 1F20; 10-OCT-01.
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DOMAIN 17 99
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PDB; 1QAU; 06-MAR-00
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Pfam; PF00667;
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953 P -> A (IN REF. 2
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311 A -> V (IN REF. 2
160559 MW; 7255CSAE16520
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Best Local Similarity 100.
Matches 10; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 29, 2003, 08:31:47 ; Search time 74 Seconds (without alignments) 1887.117 Million cell updates/sec Run on:

US-10-031-146-2 1048 1 TIKEMPQPKTFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048 Title: Perfect score: Sequence:

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Word size :

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Post-processing: Listing first 45 summaries

Databas

aneseq_101002:* SIDS2/gcgdata/geneseg/genesegp-embl/Aa1980.DaT:*	(SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*	SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*	SIDS2/gcgdata/geneseg/genesegp-embl/AA1984.DAT:*   SIDS2/gcgdata/geneseg/genesego-embl/AA1985_DAT:*	SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*	'SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*	'SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*	/SIDS2/gcgdata/geneseg/genesegp-embl/AA1991.DAT:*	'SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*	'SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*	'SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*	'SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*	'SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*	'SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*	'SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*	'SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*	'SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*	'SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*	/SIDS2/qcqdata/qeneseq/qeneseqp-emb1/AA2002.DAT:*
A_Geneseq_101002:* : /SIDS2/qcqdata/gene	/SIDS2/gcgdata/gene	/SIDS2/gcgdata/gene	/SIDS2/gcgdata/gene /SIDS2/gcgdata/gene	/SIDS2/gcgdata/gene	/SIDS2/gcgdata/gene	/SIDS2/gcgdata/gene	: /SIDS2/gcgdata/gen	: /SIDS2/gcgdata/gen	`	: /SIDS2/gcgdata/gen	`.	`		: /SIDS2/gcgdata/gen						
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result		& Ouery	% Ouerv			
	Score	Match	Length	BB	QI	Description
	1048	100.0	1048	22	AAB31978	Amino acid sequenc
7	1048	100.0	1048	22	AAB46855	B. megaterium cvto
٣	1048	100.0	1048	22	AAB46856	B. megaterium cyto
4	1048	100.0	1049	21	AAY93566	Amino acid sequenc
2	1048	100.0	1049	22	AAB31882	Amino acid sequenc
9	196	91.7	1048	22	AAB31979	Amino acid sequenc
7	860	82.1	1048	22	AAB31980	Amino acid sequenc
æ	860	82.1	1048	22	AAB31981	Amino acid sequenc
6	846	80.7	1049	22	AAY72208	Bacillus medateriu
9	266	25.4	1085	12	AAR11604	P450 17-alpha/P450

B. megaterium P-45 Cytochrome-P450-ox Human reductase am B. bassiana POPS r Human derived cyto Human derived cyto	Mouse ischaemic co Sequence of rabbit Human full-length Rabbit NADH cycoch Human contig polyp	Sequence of yeast Mitochondrial cyto Drosophila melanog Helianthus tuberos Helianthus tuberos S. epidermidis ope	Staphylococcus epi Poppy cytochrome P Poppy cytochrome P Sequence of all or Rat neuronal nitri Rat neuronal nitri Neuronal nitri	Amino acid sequenc Human nitric oxide Rat penlle neurona Human neuronal nit Drosophila melanog Candida tropicalis Candida tropicalis Drosophila melanog Candida tropicalis Candida tropicalis Candida tropicalis Candida tropicalis
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## ALIGNMENTS

Cytochrome P450 monooxygenase; oxidization; indole; indigo; indorubicin. Amino acid sequence of a Bacillus P450 monooxygenase protein. AAB31978 ID AAB31978 standard; Protein; 1048 AA. 15-MAY-2001 (first entry) AAB31978; RESULT 1

27-JUL-2000; 2000WO-EP07253. Bacillus megaterium. WO200107630-A1. 01-FEB-2001 

27-JUL-1999; 99DE-1035115. 18-NOV-1999; 99DE-1055605. 22-MAR-2000; 2000DE-1014085. (BADI ) BASF AG.

Schwaneberg U, Schmitt J, Fischer M, Schmid R; Hauer B, Pleiss J, Li Q;

WPI; 2001-182800/18. N-PSDB; AAF54832.

Cytochrome P450 monooxygenase for oxidizing organic compounds, useful

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                                         The present sequence represents a cytochrome P450 monooxygenase. The specification describes a modified cytochrome P450 monooxygenase which can oxidize at least one of the following types of substrates: optionally substituted mono- or poly-cyclic aromatic heterocyclics containing nitrogen, sulpiur or poly-cyclic aromatic heterocyclics poly-cyclic aromatics; linear or branched alkanes or alkenes; or optionally substituted cycloalkanes or cycloalkenes. The modified cyclohrome P450 monooxygenase are specifically used to oxidize indole to indigo and indorubicin. However, they may be used to oxidize many other substrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TIKEMPOPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSORLIKE
                                                                                                                                                                                                                                                                                              ACDESRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMV
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especially for converting indole to indigo, has wide substrate range
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                   Length 1048;
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100.0%; Pred. No. 0;
Live 0; Mismatches
                       54pp; German.
                                                                                                                                                                                                                         Matches 1048; Conservative
                       Claim 3; Page 35-39;
                                                                                                                                                                            1048 AA;
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                                                                                                                                                                             Sequence
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This invention describes a novel electron donor system (M1) that transfers electrons to an enzyme with redox properties comprising an inorganic, not electrode-bound, electron sink and a mediator which enable the electron transfer. The invention also describes (1) transferring (M2) oxygen to a hydrocarbon containing hydrogen donor molecule is in a reaction mediator where the hydrogen donor molecule is in a reaction mediator where the cransferring enzyme and (M1) in the presence of oxygen and incubating under suitable reaction conditions; (2) the enzymatic production (M3) of terminally or subterminally hydroxylated (position omega-1 to omega-4) catty acids comprising; (i) mixing a hydroxylatable fatty acid or fatty acid derivative in the presence of (M1) and cytochrome P450 monooxygenase; and (ii) isolating the hydroxylated product; (3) a concactor useful for the production of omega-hydroxylated fatty acids as described in (2); and (4) detecting (M4) fatty acid-monooxygenases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  system; bioreactor; acid-monooxygenase.
                                                                            QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM
                                                                                                                           VGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL
                                                                                                                                            HTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytochrome P450 monooxygenase; BM-3; electron donor electron transfer; hydroxylatable fatty acid; fatty
                                                                                                                                                                                                                                                        HQVSEADARLWLQQLEEKGRYAKDVWAG 1048
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         label in (M1); and (ii) qualitatively or quantitatively detecting the signal. The invention is useful for the production of omega-hydroxylated fatty acids and the detection of fatty acid monoxygenases. The invention provides an alternative electron donor system of enzymes with redox properties that is cheaper and more efficient, where the enzyme
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 acid or a derivative comprising a terminal chromophore or fluorescent
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This invention describes a novel modified cytochrome P450 (I) having, as a result of site-specific mutagenesis of its substrate-binding domain, an altered substrate profile, relative to the wild-type, when used for terminal and/or subterminal enzymatic hydroxylation of aliphatic carboxylic acids. The invention also describes (1) nucleic acid (II) encoding (I), and its complement, (2) expression assette (EC) containing (II) and control elements; (3) a vector containing at least one EC; (4) recombinant microorganisms transformed with at least one vector of (3); and (5) enzymatic production of terminally and/or subterminally and (5) enzymatic production of terminally and/or subterminally and (4), or isolated (I). (I), and recombinant cells that express them, are used to produce hydroxylated aliphatic carboxylic acids or their derivatives (esters and amides). (I) have altered substrate specificity, especially for hydroxylation of 8-12C fatty acids at the omega-1, 2 and/or 3 positions, and may also have increased reactivity and/or
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                                                                                   HTAFSRMPNOPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADV 1020
VGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL 960
                   VGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL
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                 TIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Process for oxidizing acyclic or cyclic terpenes, cycloalkenes, or derivatives for preventing or treating infection in human or animal body comprises mutant haem-containing enzyme which has substitution of amino acid in the active site -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes a process for oxidizing an acyclic or cyclic terpene, a cycloalkene, or a derivative. The process comprises oxidizing the compound with a mutant haem-containing enzyme which comprises a substitution of an amino acid in the active site by an amino acid with a less polar side-chain. The process is useful for oxidizing an acyclic or cyclic terpene, a cycloalkene, or their derivatives. The process is also useful for producting an oxidation product useful for preventing or treating infection in a human or animal body. The present sequence represents the amino acid sequence for use in the process of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TIKEMPOPKTFGELKNLPLLNTDKPVOALMKIADELGEIFKFEAPGRVTRYLSSORLIKE
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                                                                                            haem-containing enzyme; mutant; oxidation;
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                                                                 Amino acid sequence of the P450-BM3 sequence
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Pred. No. 0;
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                                                                                                                                                       Location/Qualifiers 303.
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100.0%;
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Best Local Similarity 100.
Matches 1048; Conservative
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                                                                                           Terpene; cycloalkene;
infection; P450-BM3.
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                                                                                                                                   Unidentified
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Cytochrome P450 monooxygenase; oxidization; indole; indigo; indorubicin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRDKTIWGDDVEEFRPERFENDSAIPQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKH
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has wide substrate
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100.0%; Pred. No. 0;
tive 0; Mismatches
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                                                                                                      27-JUL-1999; 99DE-1035115.
18-NOV-1999; 99DE-1055605.
22-MAR-2000; 2000DE-1014085.
                                                                                    27-JUL-2000; 2000WO-EP07253
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Matches 1048; Conservative
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                     Bacillus megaterium
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              PLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP
                                        PDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADR
                                               GEADASDDFEGTYEEWREHWWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMIG
                                                                               GEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG
                                                                                                                       DASQOIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVEL
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                                                                                             AFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL
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Pred. No.
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                                                                                                                  82.1%; Scc.
100.0%; Pre
0; 7
                                                      note: this sequence does nousing information provided.
                                                                                                                                                        Conservative
                                                                                                 1048 AA
                                                                                                                                          Similarity
                                           other substrates.
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368 428 428 488 488 548 548 728

728 788 788

608 608 668 668

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DDVEEFRPERFENPSAIPQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKHFDFEDHTN
                                                                                                                                     FEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHGAFSTNVVA
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                                                                                                                                                                                                                                                                                                                                                                                                                   PFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITLHTAFSRMP
                                                                                                                                                                                                                                 YELDIKETLTLKPEGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNTPLLVLYGS
                                                                                                                           NMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHPPDNAKQFV
                                                                                                                                                                       DWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDD
                                                                                                                                                                                                                                                                                                            EAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLEKQA
                                                                                                                                                                                                                                                                                                                                                          YKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEKQASITVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                              halogenated aromatic compound; electron transfer; putidaredoxin; putidaredoxin reductase; detoxification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus megaterium monooxygenase enzyme homologue, P450BM-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oxidation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monooxygenase enzyme; P450BM-3 homologue; P450cam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a modified cytochrome P450 monooxygenase. The specification describes a modified cytochrome P450 monooxygenase which can oxidize at least one of the following types of substrates: optionally substituted mono or poly-cyclic aromatic heterocyclics containing nitrogen, sulphur or oxygen; optionally substituted mono or poly-cyclic aromatics; linear or branched alkanes or alkenes; or optionally substituted cycloalkanes or cycloalkanes to indige and indorublein. However, they may be used to oxidize many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 KQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDELMVLIPQLHRDKTIWG 368
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                                                                                                                            indole; indigo; indorubicin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              organic compounds, useful has wide substrate range
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                                                                                                  Amino acid sequence of a modified P450 monooxygenase protein.
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100.0%; Pred. No. v,
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            P450 monooxygenase for oxidizing for converting indole to indigo,
                                                                                                                         P450 monooxygenase; oxidization;
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                                                                                                                                                                                             'note- "wild type Ala
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                                 standard; Protein; 1048
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99DE-1055605.
2000DE-1014085.
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                                                                              (first entry)
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hes 860; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page -; 54pp;
                                                                                                                                                                                                                                                                                                                                                                                                     B, Pleiss J,
                                                                                                                                                Bacillus megaterium
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18-NOV-1999;
                                                                             15-MAY-2001
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                                                                                                                           Cytochrome
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                                AAB31981
                                                       AAB31981;
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HTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADV 1020
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                                                                                                                                                                                                                                                                          The protein is a fusion of bovine adrenal cytochrome P450 17-alpha and Bacilius megaterium-derived cytochrome P450 BM-3. The fusion protein has the monoatomic oxygenation activity of the former and the reductivity supplying activity of the latter. Plasmid p(alphaBMI),
PDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADR
                                                               GEADASDDFEGTYEEWREHMWSDVAAYFNLD1ENSEDNKSTLSLQFVDSAADMPLAKMHG
                                                                              DASQQIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVEL
                                                                                                                                                                                                             VGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL
                                                                                                                            661 AFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     idase coding gene - has both mono-atomic bovine adrenal cytochrome p450 17-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adrenal; cytochrome P450; oxidase; reductase; steroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HQVSEADARLWLQQLEEKGRYAKDVWAG 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P450 17-alpha/P450 BM-3 fusion protein.
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                                                                                                                                                                                                                                                The present invention relates to a process for enzymatically oxidising the halogenated aromatic compounds such as 1,2-dichlorobenzene, 1,2,4-trichlorobenzene, 3,3'-dichloroblenzene, 2,2',4,5',5'-pentachloroblenzene, 3,3'-dichloroblenzene compounds and its physiolophenyl. The process comprises treating the polluted environment with a monooxygenase enzyme, P450cam, and its physiological electron transfer partners, putidaredoxin and putidaredoxin reductase, are used to oxidise the halogenated aromatic compounds. Also mutents of the monooxygenase enzyme with substitutions in the active site have enhanced oxidation activity. The process and the transgenic plant or animal which expresses the monooxygenase enzyme are used for detoxifying the environment polluted with the halo aromatic compounds. The present sequence is a Bacillus megaterium monooxygenase enzyme, P450LNH-3, which is homologous to the monooxygenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRDKTIWGDDVEEFRPERFENPSAIPQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKH 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNT 480
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                                                                                                                                                         environments contaminated with halo treating the affected area with a
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                       Disclosure; Page 32-39; 42pp; English
                                                                                                                                                                       aromatic compounds comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.8%;
Matches 1046; Conservative
                                            ISIS INNOVATION LTD.
             99GB-0014373
                                                                                                                                                        New process for detoxifying
                                                                                                                                                                                           monooxygenase enzyme
                                                                                                         WPI; 2001-071397/08
                                                                         Wong LL, Jones JP;
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                                                                                                                           N-PSDB; AAD02365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enzyme, P450cam.
             18-JUN-1999;
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present sequence represents a B, megaterium P-450BM-3 peptide fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The primers given in AAO79915-19 were used for the PCR amplification of A. niger ATCC 1015 chromosomal DNA. These degenerate primers are based on conserved sequences in known cytrochrome-P450-oxidoreductases. The DNA sequence of an isolated clone, given in AAO79914, encodes a cytochrome-P450-oxidoreductase having the sequence given in AAR66738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant DNA mol. encoding cytochrome P450 oxido:reductase esp. isolated from filamentous fungi, useful for increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 693;
                                                                              Length 17;
                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van GORCOM RFM;
                                                                                DB 20; I
2.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16; L
8.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monooxygenase.
                                                                              1.6%; Score 17; DB 100.0%; Pred. No. 2.6 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.4%; Score 15; DB 100.0%; Pred. No. 8.7 [ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                597 AA.
                                                                                                                                                                                                                                                                                                            ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        monooxygenase enzymatic conversion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Van GORCOM RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig. 2; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NEDE ) NEDERLANDSE ORG TOEGEPAST.
                                                                                                                                                                                                                                                                                                          AAR66738 standard; Protein; 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytochrome-P450-oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                Cytochrome-P450-oxidoreductase
                                                                                                                                                                259 ITFLIAGHETTSGLLSF 275
                                                                                                                                                                                                      17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    899 IMVGPGTGVAPFRGF 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93NL-0001025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-NL00135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus niger ATCC 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB49682 standard; Protein;
                                                                                                                                                                                        1 ITFLIAGHETTSGLLSF
                                                                          Query Match 1.6%
Best Local Similarity 100.C
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.4
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-036481/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             693 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van DEN BRINK JM,
                                          17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ79914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9429453-A
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                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB49682;
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AAB49682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides an isolated, mutated Monoamine Oxidase B (MAO B) enzyme having at least one amino acid substitution for wild-type amino acids in a MAO B active site, the wild-type amino acid residues selected from Phe423, Glu427 and Thr428. A plasmid containing the DNA encoding the mutated MAO B and regulatory elements can be used for the recombinant regulation of the enzyme. The mutated MAO B enzyme is useful for indirect regulation of cellular neurotransmitters and vasoamines, as the substitutions reduce MAO B's activity and alters its pH profile. The
                                                                                                                                                                                                                                                                    865
                                                                                                                                                                                                                                                                                                          887
                                                                                                                                                                                                                                                                                                                                                                                        947
                                                                                                                                                                                                                                                 YYSISSSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSE
                                                                                                                                                                                                                                                                                                                                                                                        FTLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQE
                                                                                                                                                                                                                          768 AAKTVCPPHKVELEALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPR
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutation; MAO B; cellular neurotransmitter;
                     used to transform Saccharomyces cerevisiae. The transformant is designated AH22(p(alphaBM-1)) and can be used for the synthesis of
                                                                                                                                                                                      ö
                                                                                                                                           Length 1085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New mutant enzyme useful for regulation of neurotransmitters
                                                                                                                                                                                   Indels
encoding the fusion
                                                                                                                                 Score 266; DB 12; 1
Pred. No. 5.9e-260;
                                                                                                                                                                                        ö
                                                                                                                                                        100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B. megaterium P-450BM-3 peptide fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVEATLMKSYADVHQVSEADARLWLQ 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1046 AVEATLMKSYADVHQVSEADARLWLQ 1071
  the recombinant sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; P-450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY27545 standard; peptide; 17
                                                                                                                                           25.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0077482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                        Best Local Similarity 100.
Matches 266; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoamine Oxidase; MAO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RERE-) RES DEV FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lewis DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-561665/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus megaterium
                                                                                                   1085 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vasoamine; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09946297-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-1999
  containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abell CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8001
                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                        828
                                                                                                                                                                                                                                                                                                                                              998
                                                                                                                                                                                                                                                                                                                                                                                      888
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                                                                                                                                         Query Match
                                                             steroids
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Gaps

us-10-031-146-2.rag

Beauveria bassiana.

DE19814528-A1

07-0CT-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to DNA sequence AAF29129 which encodes a human reductase represented in AAB49682. The DNA sequence shows homology with nucleotide sequences of cytochrome p450 reductases and nitric oxide synthases. The protein is related to members of the FNR gamily of flavoproteins. This reductase gene maps to human chromosome 9. The reductase polypeptide and polynucleotide are useful in screening assays, particularly as diagnostic reagents for detecting abnormally decreased or
                                                        6
                                                  Human; reductase; flavoprotein; cytochrome p450 reductase; chromosome nitric oxide synthase; cancer; drug bloactivation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated reductase polypeptides and polynucleotides, useful in screening assays, particularly for diagnosing a disease associated wisltered levels of reductase and as vaccines to protect an individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POPS; 2-phenoxypropionic acid; 2-(4-hydroxyphenoxy) propionic acid; herbicide intermediate; hydroxylation rate; reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13; DB 22; 1
Pred. No. 0.00081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                 Human reductase amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B. bassiana POPS reductase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 25-26; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY33673 standard; Protein; 700 AA
                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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100.0%;
                                                                                                                                                                                                                      13-JUN-2000; 2000WO-US16245.
                                                                                                                                                                                                                                                           99US-0334490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       against these diseases
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-112221/12.
N-PSDB; AAF29129.
                                                                                                                                                                                                                                                                                                                                  Powell DJ, Tew DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 597 AA;
                                                                                                                                             WO200077180-A1.
                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                         16-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JAN-2000
                                                                                                                                                                                 21-DEC-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
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g
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2-(4-hydroxyphenoxy) propionic acid (I) from 2-phenoxypropionic acid (POBS) or its salts. The method comprises a microorganism containing at least one of the genes contained within a Beauveria bassiana genomic sequence of 11292 bp (I), with two open reading frames. (I) is useful as a herbicide intermediate. Microorganisms containing multiple copies of (I) have significantly increased hydroxylation rates. This sequence represents the Beauveria bassiana POPS reductase described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytochrome P450 monooxygenase; cytochrome P450 reductase; NPR; pigment production; indole; dye; cosmetic industry; marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                 This invention describes a novel method for the production of
                                                                                                                                                                                                                   Production of 2-(4-hydroxyphenoxy) propionic acid from
2-phenoxypropionic acid using microorganism having increased
hydroxylation rate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Devoss J, Guengerich FP, Volkov A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13; DB 20; Length 700;
Pred. No. 0.00093;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                      Van Zeijl C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human derived cytochrome P450 reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYQU ) UNIV QUEENSLAND.
(UYVA-) UNIV VANDERBILT.
(CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                        Example 5; Page 28-31; 36pp; German.
                                                                                                                                                      Van Gorcom R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB73901 standard; Protein; 677 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              1.2%; Sco.
100.0%; Pre
0;
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                                                                          98DE-1014528
                                                                                                  98DE-1014528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          899 IMVGPGTGVAPFR 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.2
Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                     Hauer B, Dingler C,
                                                                                                                                                                             WPI; 1999-552253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                               700 AA;
                                                                                                                                                                                            N-PSDB; AAZ23663
                                                                                                                            (BADI ) BASF AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200114565-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                  01-APR-1998;
                                                                          01-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB73901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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The present sequence is cytochrome P450 reductase. The invention relates to a method for producing pigment using cells containing cytochrome P450 sequences. It involves the use of genetic material encoding a cytochrome P450 protein or a functional derivative or homologue of it in the generation of a genetically modified cell. The cell has the capacity to produce a pigment in the presence of indole, or a precursor, analogue or derivative of indole, upon expression of the genetic material. Pigment from plant or plant material is useful in the dye or cosmetic industry or as commercial tags or as markers for transformation of microbial, plant or animal cells.
                                                                 Generation of genetically modified cell to produce pigment
                                                                                                                  Claim 39; Page 145-148; 178pp; English.
WPI; 2001-257635/26.
N-PSDB; AAF76960.
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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ö Gaps ö Query Match 1.1%; Score 12; DB 22; Length 677; Best Local Similarity 100.0%; Pred. No. 0.0093; Matches 12; Conservative 0; Mismatches 0; Indels

899 IMVGPGTGVAPF 910

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529 IMVGPGTGVAPF 540

Search completed: May 29, 2003, 08:41:38 Job time: 78 secs

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(without alignments)
1063.284 Million cell updates/sec
                                                                                                                                                                                                             US-10-031-146-2
1048
1 TIKEMPQPKTFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048
                                                                                                                           May 29, 2003, 08:27:11 ; Search time 29 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                 262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                    OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                           Word size :
                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                            Sequence:
                                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2\_6/ptodata/1/laa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/5B\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/pcTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/laa/pcTUS\_COMB.pep:\*

Issued\_Patents\_AA:\*

Database :

## 14, Appl 4394, Ap 2, Appli Appl Appli Appli Appli Appli Appli Appli Sequence 30, Appl Sequence 20, Appl Description Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence sedinence sedine Sequence US-09-134-001C-4394 US-07-642-002-2 US-08-365-486A-13 US-09-010-998-5 US-09-220-574-4 US-08-365-486A-21 US-09-123-708-4 US-09-627-216A-14 US-08-319-866-11 SUMMARIES Query Match Length Score Result No.

TELEFAX: (732)594-4720 INFORMATION FOR SEQ ID NO: 30:

: 20 amino acids amino acid

TYPE: amino a STRANDEDNESS: TOPOLOGY:

single

linear

; MOLECULE TYPE: peptide US-09-057-897-30

SEQUENCE CHARACTERISTICS LENGTH: 20 amino acid

App]

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Gaps

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1.9%; Score 20; DB 4; Length 20; 100.0%; Pred. No. 1.8e-12; tive 0; Mismatches 0; Indels

216 VDKIIADRKASGEQSDDLLT 235 

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Sequence

US-09-123-708-2 US-09-123-624-2

Conservative

Query Match Best Local Similarity Matches 20; Conserv

28 8 0.8 406 6 5212296-6 30 8 0.8 412 1 US-08-102-653-11 Sequence 3 0.8 6 0.8 412 1 US-08-102-653-11 Sequence 3 0.8 6 0.8 412 1 US-08-102-653-11 Sequence 3 0.8 504 1 US-08-12-12-40A-25 Sequence 3 0.8 505 4 US-09-126-416A-229-25-25-29-46-564-16 Sequence 3 0.8 505 4 US-09-126-410A-229-29-29-20-25-29-29-29-29-29-29-29-29-29-29-29-29-29-	disk patible -DOS/MS-DOS elease #1.0, Version #1. A: US/09/057,897 ION: 36,545 MATION: 3905
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn DOUCETTILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674

LENGTH: 629
                                                                           APPLICANT: Sariasiani, Sima F
APPLICANT: Tang, Xiao-Song
APPLICANT: Tang, Xiao-Song
APPLICANT: Tang, Xiao-Song
APPLICANT: Oi, Wei Wei
APPLICANT: Gatenby, Anthony
TITLE OF INVENTION: Bioproduction of para-Hydroxycinnamic Acid
FILE REFERENCE: BC1009 US NA
CURRENT APPLICATION NUMBER: US/09/627,216A
CURRENT FILING DATE: 10999-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 629;
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0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.0%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 0.3 Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.0%; Score 10; DB
100.0%; Pred. No. 0.3
:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Staphylococcus epidermidis US-09-134-001C-4394
                       Sequence 14, Application US/09627216A Patent No. 6368837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/07642002
Patent No. 25868465
GENERAL INFORMATION:
APPLICANT: Bredt, David S.
APPLICANT: Hwang, Paul M.
APPLICANT: Reed, Randall
APPLICANT: Snyder, Solomon H.
                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Helianthus tuberosus
                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  826 PRYYSISSSP 835
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                                                              GENERAL INFORMATION:
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US-09-134-001C-4394
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-627-216A-14
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Patent No. 5801024
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
COMPUTER READABLE FORM:
MUMBER OF SEQUENCES:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Amino acid sequence containing conserved site of COTHER INFORMATION: Bacillus megaterium P-450BM3 US-09-265-653-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.6%; Score 17; DB 4; Length 17; 100.0%; Pred. No. 1.4e-09; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,279
                                  Sequence 20, Application US/09265653
Patent No. 6451570
GENERAL INFORMATION:
APPLICANT: Abell, Creed W.
APPLICANT: Lewis, Duane A.
TITLE OF INVENTION: Mutants of Monoamine Oxidase B.
FILE REFERENCE: D6048
CURRENT APPLICATION NUMBER: US/09/265,653
CURRENT FILING DATE: 1999-03-10
EARLIER APPLICATION NUMBER: US 60/077,482
BARLIER PILING DATE: 1998-03-11
NUMBER OF SEO. ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.5e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: EP PCT/NL94/00135
INFONMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.4%; Scur
100.0%; Pre
0;
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ORGANISM: Bacillus megaterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 693 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.6%
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
ses 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
RESULT 2
US-09-265-653-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-08-553-279-2
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                                                                                                                                                                                                                                                                                         SEQ ID NO 20
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1172 PRYKSISSSP 1181
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COUNTRY: USA
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MOLECULE TYPE: protein
US-08-319-866-11
                                                                                                                                              , MOLECULE TYPE: protein US-08-365-486A-13
                                                                                                                                                                                                                                                                                     826 PRYSISSSP 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 826 PRYYSISSSP 835
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                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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TITLE OF INVENTION: Purification and Molecular Cloning of Nitric TITLE OF INVENTION: Oxide Synthase NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: One Thomas Circle, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.0%; Score 10; DB 1; Length 1429;
100.0%; Pred. No. 0.79;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/08365486A

Patent No. 5814306

GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patchtin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,002
FILING DATE: 19910118
CLASSIFICATION: 435
                                                                                                                                                                                   COMPUTER READABLE FORM:
MADIUM TYPE: Floppy disk
CMDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET UNMBER: 1107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 296-5500
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1429 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-07-642-002-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMINO ACID
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Matches 10; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                      USA
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                                                                                                                                              COUNTRY: US
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
CITY: Pa
STATE: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                STATE:
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TELERAK: (415) 242-0860

TELERAK: (415) 242-08
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DB 2; Length 1430;
0.79;
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APPLICANT: Snyder, Solomon
APPLICANT: Snyder, Solomon
APPLICANT: Jaffrey, Samie
APPLICANT: Jaffrey, Samie
APPLICANT: Eliasson, Mikael
APPLICANT: Cohen, No. 6103872m
TITLE OF INVENTION: CAPON, a protein that binds
TITLE OF INVENTION: neuronal nitric oxide synthase
NUMBER OF SEQUENCES: 8
CORRESPEDUBENCE ADDRESS:
ADDRESSE: ADDRESSE:
ADDRESSE: Banner & Witcoff
STREET: 1001 G Street, NW
                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/705,625
FILING DATE: 30-AUG-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.57071
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATIS FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.0%; Score 10; DB 100.0%; Pred. No. 0.7 tilve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US/09/010,998
22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09010998 Patent No. 6103872
                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1430 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.03
Best Local Similarity 100.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1172 PRYYSISSSP 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
              ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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STATE: D
COUNTRY:
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US-09-010-998-5
COUNTRY:
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100.0%; Pred. No. 0.79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08705625
Patent No. 5908756
GENERAL INFORMATION:
APPLICANT: Supder, Solomon H.
APPLICANT: Jaffrey, Samite R.
TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric TITLE OF ENVENTION: Oxide Synthase
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                           GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                           3: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38.615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMUNICATION INFORMATION:
TELEPRONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                               Sequence 13, Application US/08880342
Patent No. 6218179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Banner & Witcoff
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Best Local Similarity 100.
Matches 10; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger
STREET: 350 Cambridg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    826 PRYYSISSSP 835
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                                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                             USA
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Gaps

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0; Indels

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GENERAL INFORMATION:
APPLICANT: SCHRADER, Juergen
APPLICANT: GOEDBECKE, Axel
TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
TITLE OF INVENTION: TREATHENT OF VASCULAR DISORDERS
FILE REFERENCE: 511169-2003
CURRENT APPLICATION NUMBER: US/09/123,708
    Gaps
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    Indels
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                                                                                                                                                                             Sequence 21, Application US/08365486A
Patent No. 5834306
GENERAL INFORMATION:
APPLICANT: Webstric, Namette H.
APPLICANT: Bishopric, Namette H.
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 21:
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Pred. No. 0.79;
0; Mismatches
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                       SEE: Dehlinger & Associates
: 350 Cambridge Avenue, Suite 250
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 1998-07-28
EARLIER APPLICATION NUMBER: 08/553,503
EARLIER FILING DATE: 1996-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: P4411402.8 EARLIER FILING DATE: 1994-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-123-708-4
; Sequence 4, Application US/09123708
; Patent No. 6146887
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Best Local Similarity 100.
Matches 10; Conservative
  10; Conservative
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                                                                  1172 PRYYSISSSP 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                          826 PRYYSISSSP 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: CA
                                                                                                                                                                    US-08-365-486A-21
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    Matches
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                                                                                                                                                                                                                                                                                                                              Length 1430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Snyder, Solomon H.
APPLICANT: Jaffrey, Samie R.
TITLE OF INVENTION: Drotein Inhibitor of Neuronal Nitric
TITLE OF INVENTION: Oxide Synthase
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Banner & Witcoff
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/220,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.0%; Score 10; DB 4;
100.0%; Pred. No. 0.79;
                                                                                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                            Score 10; DB 3;
Pred. No. 0.79;
                                                                                                                                                                                                                                                                                                                            Query Match 1.0%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 0.7 Matches 10; Conservative 0; Mismatches
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                                        01107.73424
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APPLICATION NUMBER: 08/705,625
FILING DATE: 30-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.57
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09220574
Patent No. 6168926
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6103872e
US-09-010-998-5
                                                                                                                                         INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1430 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens US-09-220-574-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: NO
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-09-220-574-4
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Search completed: May 29, 2003, 08:32:17 Job time : 30 secs

1176 PRYSISSSP 1185

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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using sw model OM protein - protein search,

May 29, 2003, 08:30:56; Search time 54 Seconds (without alignments) 1964.489 Million cell updates/sec Run on:

US-10-031-146-2 1048 1 TIKEMPQPKTFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048 Title: Perfect score:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

Sequence:

383519 seqs, 101223694 residues Searched:

0 Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

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14: /cgn2\_6/ptodata/2/pubpaa/USO0\_PUBCOMB.pep:\* Published\_Applications\_AA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	, Appl	Appli	Appl,	-	, Appl		~	, Appl	7, App	8, App	, Appl	, Appl	7, App	118, App	, Appl			-	
uo	20	7	23	е 1	14	e 4	83	84	117,	11	83,	84				84,			83,
Description	Sequence 20, Appl	Sequence 2, Appli	Sequence 23,	Sequence 14	Sequence 14,	Sequence	Sequence 83,	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
ΩI	US-10-119-604C-20	US-09-778-319-2	US-09-371-347-23	US-09-765-873A-14	US-10-224-249-14	US-09-740-046-4	US-10-138-838-83	US-10-138-838-84	US-10-138-838-117	US-10-138-838-118	US-10-139-031-83	US-10-139-031-84	US-10-139-031-117	US-10-139-031-118	US-10-138-905-83	US-10-138-905-84	US-10-138-905-117	US-10-138-905-118	US-10-138-916-83
DB	6	6	6	10	6	10	6	σ	6	σ	6	0	σ	6	6	6	σ	σ	6
% Query Watch Length DB	17	597	677	588	1433	516	619	619	619	619	619	619	619	619	619	619	619	619	619
& Query Match	1.6	1.2	1.1	1.0	1.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	0.9
Score	17	13	12	10	10	თ	σ	σ	σ	6	თ	თ	თ	σ	σ	σ	σ	6	6
Result No.	1	7	٣	4	Ŋ	9	7	80	σ	10	11	12	13	. 14	15	16	17	18	19

Sequence 84, Appl Sequence 117, App Sequence 118, Appl Sequence 84, Appl Sequence 117, App Sequence 117, Appl Sequence 117, Appl Sequence 124, Appl Sequence 12, Appl Sequence 44, Appl Sequence 46, Appl Sequence 46, Appl Sequence 47, Appl Sequence 41, Appl Sequence 44, Appl Sequence 49, Appl Sequence 49, Appl Sequence 41, Appl Sequence 21, Appl Sequence	day (FTZ companies)
9 US-10-138-916-84 9 US-10-138-916-118 9 US-10-138-916-118 9 US-09-976-800-83 9 US-09-976-800-117 9 US-09-976-800-117 9 US-09-976-800-118 10 US-09-911-781-11 10 US-09-911-781-11 10 US-09-911-781-12 11 US-09-911-781-12 12 US-09-911-781-12 13 US-09-917-48 9 US-09-971-347-48 9 US-09-371-347-48 9 US-09-371-347-48 9 US-09-371-347-48 9 US-09-371-347-48 9 US-09-371-347-48 9 US-09-371-347-48 9 US-09-371-347-48 9 US-09-371-347-41 9 US-09-371-347-41 9 US-09-371-347-42 9 US-09-371-347-42 9 US-09-371-347-44 9 US-09-371-347-44 9 US-09-371-347-44 9 US-09-371-347-44 9 US-09-371-347-44 9 US-09-371-347-44 9 US-09-371-347-44 9 US-09-371-347-44 9 US-09-371-347-44 9 US-09-371-347-42 9 US-09-371-347-44 9 US-09-371-347-44 9 US-09-371-347-44	1
679 679 679 679 679 679 679 679 882 682 683 698 698 698 698 698 698 698 698 698 698	,
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# ALIGNMENTS

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Gaps
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                                                                                        APPLICANT: Abell, Creed W.
APPLICANT: Lewis, Duane A.
TITLE OF INVENTION: Mutants of Monoamine Oxidase B.
FILE REFERENCE: D6048/D
CURRENT APPLICATION NUMBER: US/10/119,604C
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: US 09/265,653
PRIOR FILING DATE: 1998-03-10
NUMBER OF SEQ ID NOS: 27
LENGTH: 17
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1.6%; Score 17; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 5.8e-09;
Matches 17; Conservative 0; Mismatches 0;
                    Sequence 20, Application US/10119604C Publication No. US20030082772A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Bacillus megaterium FEATURE:
US-10-119-604C-20
                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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Sequence 2, Application US/09778319
Patent No. US20020155560A1
GENERAL INFORMATION
APPLICANT: FOWLL, DAVID J.
APPLICANT: TEW, DAVID G.
TITLE OF INVENTION: A REDUCTASE
FILE REFERENCE: GH-70627-C1
CURRENT APPLICATION NUMBER: US/09/778,319 1 ITFLIAGHETTSGLLSF 17 US-09-778-319-2 g

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365 PRYYSISSSP 374 ·
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ORGANISM: Homo sapiens
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APPLICANT: EXELIXI
     US-09-765-873A-14
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US-09-740-046-4
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| Publication No. US20030082676A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION: CLONINO, AND METHODS FOR EVALUATING RISK OF NEURAL TITLE OF INVENTION: CLONINO, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
| TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
| TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
| TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
| TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
| TITLE OF INTERPRETATION NUMBER: 05/09/371,347
| CURRENT APPLICATION NUMBER: 06/071,622
| PRIOR FILING DATE: 1999-01-16
| PRIOR FILING DATE: 1999-01-15
| NUMBER OF SEQ ID NOS: 51
| SOFTWARE: FASTSEQ for Windows Version 4.0
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Patent No. US20010053847A1
GENERAL INFORMATION:
TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
FILE REFERENCE: BC1009 US CIP
CURRENT APPLICATION NUMBER: US/09/765,873A
CURRENT FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 09/627,216
PRIOR PELING DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-27
PRIOR PLING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 38
SOFTWARE: MICTOSOft Office 97
                                                                                                                                                                                                                                                                             Query Match 1.2%; Score 13; DB 9; Length 597; Best Local Similarity 100.0%; Pred. No. 0.001; Matches 13; Conservative 0; Mismatches 0; Indels
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CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 09/334,490
PRIOR FILING DATE: 1999-06-16
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
ERQ ID NO 2
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US-09-371-347-23
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SEQ ID NO 14
LENGTH: 588
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LENGTH: 677
                                                                                                                                                                            TYPE: PRT
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     TROPICALIS AND METHODS RELATING THERETO
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                                                                                                                                                                                                                                                                     0; Indels
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Pred. No. 8;
0; Mismatches
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Pred. No. 8;
0; Mismatches
 TITLE OF INVENTION: TROPICALIS AND METHOD FILE REFERENCE: 1010-16 CURRENT APPLICATION NUMBER: US/10/138,838 CURRENT FILING DATE: 2002-05-03 PRIOR APPLICATION NUMBER: US/09/976,800 PRIOR FILING DATE: 2001-10-12 NUMBER OF SEQ ID NOS: 118 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 117, Application US/10138838
Publication No. US20030049821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 118, Application US/10138838 Publication No. US20030049821A1 GENERAL INFORMATION:
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100.0%; Pre
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100.0%; Pre
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; ORGANISM: CANDIDATROPICALIS
US-10-138-838-117
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US-10-138-838-84
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APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
                                                                                                                                                                                                                                    Query Match 0.9
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.9
Best Local Similarity 100.
Matches 9; Conservative
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TYPE: PRI
                                                                                                                                    SEQ ID NO 84
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TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
FILLE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/138,838
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TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXXLAM
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                                                                                   Length 516;
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                                                                                   DB 10;
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100.0%; Pred. No. 8;
                                                                                Query Match 0.9%; Score 9; DB 1
Best Local Similarity 100.0%; Pred. No. 6.2
Matches 9; Conservative 0; Mismatches
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PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
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Publication No. US20030049821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  Sequence 83, Application US/10138838
Publication No. US20030049821A1
                 ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-740-046-4
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Elrich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
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Cornett, Cathy A.
Brenner, Alfred A.
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Loper, John C.
Gleeson, Martin
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; ORGANISM: CANDIDATROPICALIS
US-10-138-838-83
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APPLICANT: Craft, David L.
APPLICANT: Elrich, Dudley
APPLICANT: Eshoo, Mark
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Best Local Similarity 100.
Matches 9; Conservative
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LENGTH: 516
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APPLICANT:
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APPLICANT: LOBET, JOHN C.
APPLICANT: LOPET, JOHN C.
APPLICANT: LOPET, JOHN C.
APPLICANT: Glesson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: TROPICALIS AND PROTEINS RELATING THERETO
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
CURRENT APPLICATION NUMBER: US/10/139,031
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
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APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTRASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
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CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
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Publication No. US20030049822A1
GENERAL INFORMATION:
                                          Sequence 84, Application US/10139031 Publication No. US20030049822A1 GENERAL INFORMATION:
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Cornett, Cathy A.
Brenner, Alfred A.
                                                                                                                                                                                                    Madduri, Krishna M.
Cornett, Cathy A.
Brenner, Alfred A.
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SOFTWARE: Patentin version 3.1
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SOFTWARE: Patentin version 3.1
SEQ ID NO 117
LENGTH: 679
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Best Local Similarity 100.v
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APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
                                                                                                               APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
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LENGTH: 679
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                                                           APPLICANT: Tang, Maria
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/138,838
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR PAPLICATION NUMBER: US/09/976,800
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TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: CYTOCHROME P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
CURRENT ENERGY 1010-16
CURRENT FILLS DATE: 2001-50-50-30
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILLING DATE: 2001-10-12
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100.0%; Pred. No. 8;
tive 0; Mismatches
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APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Ocrnett, Cathy A.
APPLICANT: Tang, Maria
APPLICANT: Tang, Maria
Madduri, Krishna M.
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SOFTWARE: Patentin version 3.1
SEQ ID NO 118
LENGTH: 679
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 83
                     Cornett, Cathy A.
Brenner, Alfred A.
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US-10-139-031-83
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Best Local Similarity 100.
Matches 9; Conservative
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; ORGANISM: CAN
US-10-138-838-118
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APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
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  0.9%; Score 9; DB 9;
100.0%; Pred. No. 8;
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100.0%; Pred. No. 8;
tive 0; Mismatches
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CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.1
LENGTH: 679
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CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
                                                                                                                                                                                                                           Sequence 118, Application US/10139031 Publication No. US20030049822A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 83, Application US/10138905
Publication No. US20030068800A1
GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eirich, Mark
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Cornett, Cathy A.
Brenner, Alfred A.
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Cornett, Cathy A.
Brenner, Alfred A.
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APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
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Best Local Similarity 100.
Matches 9; Conservative
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Loper, John C.
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US-10-139-031-118
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US-10-138-905-83
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APPLICANT:
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Job time : 54 secs
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Best Local Similarity 100.0%; Pr
Matches 9; Conservative 0;
            NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.1
SEQ ID NO 83
LENGTH: 679
PRIOR FILING DATE: 2001-10-12
                                                                     ; TYPE: PRT; ORGANISM: CANDIDATROPICALIS
US-10-138-905-83
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 29, 2003, 08:28:41; Search time 297 Seconds (without alignments) 2275.018 Million cell updates/sec Run on:

US-10-031-146-2 1048 1 TIKEMPQPKTFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048 Perfect score:

Scoring table: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0

4569144 segs, 644733110 residues Searched:

0

Word size :

Total number of hits satisfying chosen parameters:

4569144

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Databas

tents_AA_Main:*	2_6/ptodata/1/paa/PCTUS 2_6/ptodata/1/paa/US06_	<pre>3: /cgn2_6/ptodata/1/paa/US07_COMB.pep:* 4: /cgn2_6/ptodata/1/paa/US080_COMB.pep:*</pre>	2_6/ptodata/1/paa/US081_COMB	2_6/ptodata/1/paa/US082_COMB.	_6/ptodata/1/paa/US083_	_6/ptodata/1/paa/US084_	_6/ptodata/1/paa/US085_	2_6/ptodata/1/paa/US086_COM	9	_6/ptodata/1/paa/US088_COMB.	_6/ptodata/1/paa/US089_COMB.	_6/ptodata/1/paa/US090_COMB.	_6/ptodata/1/paa/US091_COMB.	_6/ptodata/1/paa/US092_COMB.	: /cgn2_6/ptodata/1/paa/US093_COMB.	_6/ptodata/1/	9: /cgn2_6/ptodata/1/paa/	_6/ptodata/1/paa/US096_COMB.	<ol> <li>/cgn2_6/ptodata/1/paa/US097_COMB.</li> </ol>	2: /cgn2_6/ptodata/1/paa/US098_COMB.	3: /cgn2_6/ptodata/1/paa/US099_COMB.	_6/ptodata/1/paa/US100_COMB.	2_6/ptodata/1/paa/US101_COMB.	_6/ptodata/1/paa/US102_COMB.	2_6/ptodata/1/paa/US60_COMB.	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 2, Appli	Sequence 35, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 53927, A	Sequence 9, Appli
SUMMARIES	ΙD	US-10-031-146-2	US-10-031-241-35	US-10-031-695-2	PCT-US02-11954-2	US-09-791-537-53927	US-10-031-146-9
	DB	24	24	24	-	21	24
	Query Match Length DB ID	1048	1048	1048	1049	1049	1049
dФ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0
	Score	1048	1048	1048	1048	1048	1048
	Result No.	1	7	3	4	2	9

Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 3, Appli Sequence 3, Appli Sequence 116499, Sequence 116499, Sequence 116501, Sequence 116501, Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 139586, Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 20, Appli Sequence 2034, Appli Sequence 3234, Appli	41634 8203, 38, A
25 US-10-125-640-2 26 US-10-201-313-2 29 US-09-866-339A-21 29 US-09-866-339A-21 29 US-09-866-339A-21 20 US-09-791-537-94076 21 US-09-791-537-116499 22 US-09-791-537-116499 23 US-09-791-537-116499 24 US-09-791-537-116501 25 US-09-791-537-116501 27 US-09-791-537-116501 28 US-09-791-537-116501 28 US-09-791-537-139586 29 US-09-791-537-139588 20 US-09-791-537-139588 20 US-09-791-537-139588 21 US-09-791-537-139768 22 US-09-791-537-139768 23 US-09-791-537-139788 24 US-09-791-537-139788 25 US-09-791-537-139788 27 US-09-791-537-139788 28 US-09-791-537-149331 28 US-09-791-537-149331 28 US-09-791-537-44-3334 28 US-09-791-537-44-333	US-09-417-507-416 US-09-791-537-820 US-10-021-425-38
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## ALIGNMENTS

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RESULT 1

US-10-031-146-2

Sequence 2, Application US/10031146

Sequence 2, Application US/10031146

Sequence 2, Application US/10031146

Sequence 2, Application US/10031146

APPLICANT: HAUER, Bernhard

APPLICANT: SCHMITT, Jutta

TITLE OF INVENTION: Novel cytochrome P450 monooxygenases and their use for the oxi

TITLE OF INVENTION: Organic substrates

FILE REFERENCE: 50915

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: PCT/EP 00/07253

PRIOR FILING DATE: 2000-07-27

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Word Perfect version 6.1

SEQ ID NO 2

LENGTH: 1048

TYPE: PRT

ORGANISM: Bacillus megaterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 24; Length 1048;
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Indels

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1 TIKEMPOPKTFGELKNIPLINTDKPVQALMKIADELGEIFKPEAPGRVTRYLSSORLIKE 60

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qq	1 TIKEMPOPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSGRLIKE 60	; Sequence 35, Application US/10031241
ΟΥ Db	61 ACDESREDKNLSQALKEVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMWY 120 	; GENERAL INFORMATION: ; APPLICANT: Hauer, Bernhard ; APPLICANT: Schmid, Rolf D. ; APPLICANT: Schwaneberg, Ulrich
Οy	DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRA	; TITLE OF INVENTION: Electron donor system for enzymes and its use in the biochemic ; TITLE OF INVENTION: conversion of substrates ; FILE REFERENCE: M/40076
qa	DIAVQLVQKWERLNADEHIEVPEDMTRLTLDFIGLCGFNYRFNSFYRDQPHPFIT	; CURRENT APPLICATION NUMBER: US/10/031,241 ; CURRENT FILING DATE: 2002-05-06
oy B	181 LDEAMNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSDDLLTHMLNG 240 	; PRIOR APPLICATION NUMBER: PCT/EP00/07251 ; PRIOR FILING DATE: 2000-07-27 ; NUMBER OF SEO ID NOS: 35
δλ	KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKA'AEEAARVLVD	; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 35 ; LENGTH: 1048
Q O	KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD	ΗO
දු දු	301 PVPSYKOVKQLKYVGMVDRALREMPRAPARSIZHREDYVLGGEYPLEKGDELMYLIPQL 360 	US-10-031-241-35 Query Match 100.0%; Score 1048; DB 24; Length 1048;
Qy 4d	361 HRDKTIWGDDVEERPERFENPSALPQHAFKPFGNGQRACIGQQFALHEATLVICAMLKH 420	Best Local Similarity 100.0%; Pred. No. 0; Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps
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QQ		Qy 61 ACDESREDKNISQALKEVRDFAGDGIFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMY 120
Oy	PLLVLVGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP	Db 61 ACDESRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMWV 120
අ	81 PLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP	121 DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRENSFYRDQPHPFITSMVRA
oy Q	541 PDNAKOPYNALDOASABEVKGYRXSVFGCGGDKNATTYQKPAFIDETLAAKGAENIADR 600 	Db 121 DIAVOLVOKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDOPHPFITSMYRA 180 Qy 181 LDEAMNKLQRANPDDPAYDENKRQFQEDIKVWNDLVDKIIADRKASGEQSDDLLTHMLNG 240
. Ой	601 GEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLGFVDSAADMPLAKMHG 660	
qa	601 GEADASDDFEGTYEEWREHMWSDVAAXFNLDIENSEDNKSTLSLQFVDSAADMPLAKHIG 660	QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD 300
ð á	661 AFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL 720 661 AFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL 720 661 AFSTNVANASEROODG SABGERDHI FTET BERESKARFGARTNANNEN BARGA 720	241 KDPETGEPLDENTRYQITTFLIAGHETTSGLLSFALYFLVRNPHVLQKRAREBARVLVD
Qy		Db PVPSYKQVKQLKYVGMVLNEALRAPTAPAPSLYAKEDTVLGGEFPLEKGDELMVLIPQL 360
qa		Qy 361 HRDKTIWGDDVEEFRPERFENPSAIDQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKH 420
λo i	EALLEKOAYKEOVLAKRLTMLEILEKYPACEMKPSEFIALLPSIRPRYYSISSSPRVDEK	361 HRDKTIWGDDVEEFRPERFENPSAIPQHAFKPFGNGRACIGOOFALHEATLVLGNMLKH
e è	/81 EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKESEFIALLPSIRPRYYSISSSPRVDEK 840 841 QASITVSVVSGEAWSGYGEYKGIASNYLAELOEGDTITCFISTPOSEFTLPKDPETPLIM 900	Qy 421 FDFEDHTNYELDIKETLTLKFEGFYVKAKSKKIPLGGIPSFSTEGSAKKYRKKAENAHNT 480 
qq		481 PLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP
ογ	901 VGPGTGVAPFRGFVQARKQLKEGGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL 960	Db 481 PLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP 540
අු	901 VGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL 960	Qy 541 PDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADR 600
ò 6	961 HTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADV 1020 061	541 PDNAKQEVDWIDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADR
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OY 361 HRDKTIWGDDVEEFRPERFENPSAIPQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKH 420	Db         481 PLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP 540           Qy         541 PDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADR 600           L	QY         661 AFSTNUVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL 720           LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	781 EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEK	QY         901 VGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLXQEELENAQSEGIITL 960           1	Qy 1021 HQVSEADARLWLQQLEEKGRYAKDVWAG 1048 	RESULT 4  PCT-US02-11954-2  Sequence 2, Application PC/TUS0211954  GENERAL INFORMATION:  APPLICANT: Cirino, Patrick C.  APPLICANT: Arnold, Frances H.  TITLE OF INVENTION: PERSONIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS: FILE REFERENCE: 4058/2X23-W00  CURRENT APPLICATION NUMBER: PCT/US02/11954  CURRENT APPLICATION NUMBER: PCT/US02/11954  PRIOR PILING DATE: 2001-04-16  PRIOR PILING DATE: 2001-04-16  PRIOR PELING DATE: 2001-05-03  PRIOR APPLICATION NUMBER: 60/288,636  PRIOR PELING DATE: 2001-12-12  NUMBER OF SEQ ID NOS: 12  SOFTWARE: PATENTION OFFE: 2001-12-12  NUMBER OF SEQ ID NOS: 12  SOFTWARE: PATENTION OFFE: 2001-13-13  PRIOR PILING DATE: 2001-13-13  SOFTWARE: PATENTION OFFE: 2001-13-13  SOFTWARE: PATENTION OFFE: 2001-13-13  SOFTWARE: PATENTION OFFE: 2001-13-13  SOFTWARE: PATENTION OFFE: 2001-13-13  PRIOR PATENTION OFFE: 2001-13-13  SOFTWARE: PATENTION OFFE: 2001-13-13
721 781 781 841	OY         901 VGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL 960           111111111111111111111111111111111111	Db 1021 HQVSEADARLWLQQLEEKGRYAKDVWAG 1048  RESULT 3 US-10-031-695-2 ; Sequence 2, Application US/10031695 ; GENERAL INFORMATION:    APPLICANT: Hauer, Bernhard	APPLICANT: Pleiss, Jurgen APPLICANT: Schwaneberg, Ulrich APPLICANT: Schwaneberg, Ulrich APPLICANT: Schwaneberg, Ulrich TITLE OF INVENTION: Modified cytochrome P450 monooxygenases FILE REFERENCE: M/40434 CURRENT APPLICATION NUMBER: US/10/031,695 CURRENT FILING DATE: 2002-05-06 PRIOR APPLICATION NUMBER: PCT/FP00/07252	S ?	Query Match 100.0%; Score 1048; DB 24; Length 1048; Best Local Similarity 100.0%; Pred. No. 0; Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FKFEAPGRVTRYLSSQ FKFEAPGRVTRYLSSQ HNILLPSFSQQAMKGY HILLPSFSQQAMKGY HILLPSFSQQAMKGY FRILLPSFSQQAMKGY FRILLPSFSQQAMKGY FRILLPSFSQQAMKGY FRILLPSFSQQAMKGY FRILLPSFSSQQAMKGY FILLSFSFSQQAMKGY FILLSFSFSSQQAMCGY FILLSFSFSSQGAMCGY FILLSFSSGGAMCGY FILLSFSGGAMCGY FILLSFSGGAMCGY FILLSFSGGAMCGY FILLSFSGGAMCGY FILLSFSGGAMCGY FILLSFSGGAMCGY FILLSFSGGAMCGY FILLSFSGGAMCGY FILLSFSG

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RELEVANT RESIDUES: (1)..(1049)
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Sequence 53927, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bidonaix, Inc.
APPLICANT: Debc, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 53927
LENGTH: 1049
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QY 601 GEADASDDFEGTYEEWREHMWSDVAAXFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG 660	661 AFSTNVVASKELQOPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGI	721 DASQUIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAKTVCPPHKVEL 		QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDFETPLIM 	SILTL SILTL	YADV	1021 HQVSEADARLWLQQLEEKGRYAKDVWAG 1048		Sequence 9, 1 GENERAL INFOI APPLICANT: 1	A APPLICANT: PLEELS, JUGIGED A APPLICANT: SCHWANEBERG, Ulrich APPLICANT: SCHWITT, Jutta TITLE OF INVENTION: NOVEL cytochrome P450 monooxygenases and their use for the oxidat		PRIOR FILING DATE: 2000-07-27 NUMBER OF SEQ ID NOS: 9 SOFTWARE: Word Perfect version 6.1	LENGTH: TYPE: PE ORGANISMS-10-031-14	Query Match 100.0%; Score 1048; DB 24; Length 1049; Best Local Similarity 100.0%; Pred. No. 0; Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY         1 TIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60	Db 62 ACDESREDKNISQALKEVRDFAGDGLETSWHERNNKKAHNILLPSFSQQAMKGYHAMMY 121 QY 121 DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGENYRENSFYRDQPHPFITSWYRA 180

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                                                                                  PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank / P14779
DATABASE ENTRY DATE: 1990-04-01
RELEYANT RESIDUES: (1)..(1049)
                                                                                                                                                             0; Mismatches
                                                                                                                                         Query Match 100.0%; Score 1048; Best Local Similarity 100.0%; Pred. No. 0; Matches 1048; Conservative 0; Mismatches
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 60/340,602
PRIOR FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
                                                                  TYPE: PRT
ORGANISM: Bacillus megaterium
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APPLICANT: Farinas, Edgardo
APPLICANT: Glieder, Anton
APPLICANT: Glieder, Anton
APPLICANT: Schwanberg, Ulrich
TITLE OF INVENTION: IMPROVED CYTOCHROME P450 OXYGENASES
FILE REFERENCE: 3369/1K238-US.
CURRENT APLICATION UNBER: US/10/201,213
CURRENT FILING DATE: 2002-07-22
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank / P14779
DATABASE ENTRY DATE: 1990-04-01
RELEVANT RESIDUES: (1)..(1049)
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PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/308,429
PRIOR FILING DATE: 2001-07-27
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
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Best Local Similarity 100.
Matches 1048; Conservative
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   ; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (1)..(1049)
; OTHER INFORMATION: Coding
US-09-856-339A-21
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APPLICANT: Bell, Stephen
APPLICANT: Bell, Stephen
APPLICANT: Bell, Stephen
TITLE OF INVENTION: PROCESS FOR OXIDISING TER!
FILE REFERENCE: HO-P02196US0 (10104571)
CURRENT APPLICATION NUMBER: US/09/056,339A
CURRENT FILING DATE: 2001-05-18
PRIOR FILING DATE: 1999-11-19
PRIOR FILING DATE: 1998-11-19
PRIOR FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
SEQ ID NO 21
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ORGANISM: Bacillus
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US-09-856-339A-21
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GENERAL INFORMATION:
APPLICANT: Blonomix. Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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SEQ ID NO 94076
LENGTH: 471
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Best Local Similarity
Matches 471; Conserv
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US-09-791-537-94076
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US-09-791-537-94076
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APPLICANT: Luet, Wong
APPLICANT: Jonathan, Jones
TITLE OF INVENTION: PROCESS FOR OXIDISING AROMATIC COMPOUNDS
FILE REFERENCE: P02351051 / 10112404 / N.76277B
CURRENT APPLICATION NUMBER: US/10/018,730A
CURRENT PILING DATE: 2002-04-04
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 2000-06-19
PRIOR FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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Pred. No. 0;
0; Mismatches
                                                             HQVSEADARLWLQQLEEKGRYAKDVWAG 1048
                                                                         Sequence 4, Application US/10018730A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Bacillus megaterium
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Best Local Similarity 99.8%;
Matches 1046; Conservative
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 PVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDELMVLIPQL 360
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APPLICANT: CITION, PARTICK C.
APPLICANT: CITION, PARTICK C.
APPLICANT: Arnold, Frances H.
TITLE OF INVENTION PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS;
FILE REFERENCE: 4058/IK237-US3
CURRENT APPLICATION NUMBER: 05/24-16
PRIOR APPLICATION NUMBER: 60/284,215
PRIOR PILING DATE: 2001-04-16
PRIOR PPLING DATE: 2001-05-03
PRIOR PPLING DATE: 2001-05-03
PRIOR PPLING DATE: 2001-05-03
PRIOR PPLING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VERSION 3.1
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DATABASE ACCESSION NUMBER: GenBank / P14779
DATABASE ENTRY DATE: 1990-04-01
RELEVANT RESIDUES: (1)..(464)
                                                                                                                                                                                               Sequence 3, Application US/10125640 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Bacillus megaterium
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APPLICANT: Cirino, Patrick C.
APPLICANT: Cirino, Patrick C.
TITLE OF INVENTION PERCYLEDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS:
FILE REFERENCE: 4059/ZA237-W00
CURRENT APPLICATION NUMBER: PCT/US02/11954
CURRENT FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: 60/284,215
PRIOR PELING DATE: 2001-04-16
PRIOR PELING DATE: 2001-04-16
PRIOR PPLING DATE: 2001-05-03
PRIOR PPLING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NOS: 12
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                                                                                                                                                                        1 TIKEMPOPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSORLIKE
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                                          KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD
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100.0%; Pred. No. 0;
live 0; Mismatches
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DATABASE ENTRY DATE: 1990-04-01
RELEVANT RESIDUES: (1)..(464)
                                                                                                                                                                                                                                                                                                            Sequence 3, Application PC/TUS0211954 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 463; Conservative
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61 ACDESRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMV 120
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                                                                                                                                                                                                                                                                                                                                 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD
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                                                                                                                                                                                                       Query Match 43.4%; Score 455; DE Best Local Similarity 100.0%; Pred. No. 0; Matches 455; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            completed: May 29, 2003, 08:37:24
SOFTWARE: Patentin version 3.0 SEQ ID NO 8264 LENGTH 455
                                                                                                                                 ; ORGANISM: pdb 2BMHA
US-09-791-537-8264
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                                                                                                            TYPE: PRT
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                                                                                                                                        Sequence 116499, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Bobe, Debe, D
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Dankser, Joseph
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
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Matches 458; Conservative
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; ORGANISM: pdb 1BVYA
US-09-791-537-116499
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                                                                                                               May 29, 2003, 08:29:06; Search time 105 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                    995812 seqs, 207002235 residues
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Gapop 60.0 , Gapext 60.0
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Perfect score:
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Pending\_Patents\_AA\_Now:\*

1: /cgn2\_6/ptodata/2/paa\_PCT\_NEW\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/paa\_VUS06\_NEW\_COMB.pep:\*

3: /cgn2\_6/ptodata/2/paa\_VUS07\_NEW\_COMB.pep:\*

4: /cgn2\_6/ptodata/2/paa\_VUS07\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/paa\_VUS07\_NEW\_COMB.pep:\*

6: /cgn2\_6/ptodata/2/paa\_VUS09\_NEW\_COMB.pep:\*

7: /cgn2\_6/ptodata/2/paa\_VUS09\_NEW\_COMB.pep:\*

7: /cgn2\_6/ptodata/2/paa\_VUS10\_NEW\_COMB.pep:\*

Post-processing: Listing first 45 summaries

Database :

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 8117, Ap Sequence 2518, Ap Sequence 2517, Ap Sequence 4874, Ap Sequence 24, Appl Sequence 24, Appl Sequence 14954, Ap 572, App 23, Appl 22034, A 187294, 9867, Ap 14, Appl 14, Appl 8116, Ap 8116, Ap 2, Appli 24, Appl 14954, A 12757, A Sequence 1, Appli Sequence 13060, A 14960, A 191313, Description Sequence US-10-148-907A-23 US-10-369-493-22034 US-10-424-599-187294 US-10-424-599-191313 US-10-156-761-9867 US-10-156-761-14954 US-10-219-051B-12757 US-60-440-068-572 US-09-675-784A-13060 US-10-092-411A-4394 US-60-453-135-14960 US-10-369-493-2517 US-10-369-493-4874 US-10-369-493-7634 US-10-214-446-24 SUMMARIES Query Match Length DB 629 719 11199 11199 11199 11199 11429 1434 Score Result

Sequence 47717, A Sequence 3240, Ap Sequence 3240, Ap Sequence 3240, Ap Sequence 52887, A Sequence 3, Appli Sequence 5, Appli Sequence 6, Appli Sequence 81, Appli Sequence 117, Appli Sequence 117, Appli Sequence 118, Appli Sequence 117, Appli Sequence 117345, Sequence 117345,
US-10-425-114-47717 US-10-425-114-44757 PCT-1082-4025-3240 US-10-320-797-340 US-10-425-114-52887 US-10-272-017A-3 US-10-272-017A-5 US-10-272-017A-6 US-10-272-017A-6 US-10-272-017A-6 US-10-272-017A-6 US-10-405-660-81 US-10-405-660-117 US-10-405-660
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2000 - 20

### ALIGNMENTS

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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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100.0%; Pred. No. 9.3e-08;
tive 0; Mismatches 0; Indels
                SEQUENCE 8117, Application US/10156761
GENERAL INFORMATION:
APPLICANT: OWNTRA, SATOSHI
SAPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRA, HAROO
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: HATTORI, WASHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERBNCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-30
SEQ ID NOS: 15109
SEQ ID NO 8117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Streptomyces avermitilis US-10-156-761-8117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 TFLIAGHETTSGLLSFA 276
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-369-493-2518
US-10-156-761-8117
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APPLICANT: Cao, Tongwei APPLICANT: Cao, Tongwei APPLICANT: Cao, Tongwei APPLICANT: Cao, Tongwei APPLICANT: Slater, Steven C. APPLICANT: Slater, Steven C. APPLICANT: Goldman, Barry S. APPLICANT: Chen, Xianfeng TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE REFERENCE: 38-10(52052)8 CURRENT APPLICATION NUMBER: US/10/369,493
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APPLICANT: Wellary, Mark J.
APPLICANT: Burk, Mark J.
APPLICANT: Hitchman, Tim
APPLICANT: Hitchman, Tim
APPLICANT: Pujol, Catherine
APPLICANT: Pujol, Catherine
APPLICANT: Short, Jay M.
TITLE OF INVENTION: THEM AND METHODS OF MAKING AND USING THEM
TITLE OF INVENTION: THEM AND METHODS OF MAKING AND USING THEM
FILLE REFERENCE: 0910-500001
CURRENT APPLICATION NUMBER: US 60/309,497
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 59
SEQ ID NO 24
LENGTH: LOT7
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1.1e-05;
  1.4%; Score 15; DB 6; Length 592; 100.0%; Pred. No. 6e-06; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.4%; Score 15; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 15; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-1
NUMBER OF SEQ ID NOS: 47374
LENGTH: 592
                                                                                                                                                                                                                              RESULT 5
US-10-369-493-7634
i; Sequence 7634, Application US/10369493
; GENERAL INFORMATION:
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US-10-369-493-7634
                                                                                                       899 IMVGPGTGVAPFRGF 913
                                                                                                                                   449 IMVGPGTGVAPFRGF 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        899 IMVGPGTGVAPFRGF 913
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     Query Match
Best Local Similarity 100.0
Matches 15; Conservative
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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Gaco, Yongwei
APPLICANT: Goddman, Barry S.
APPLICANT: Goddman, Barry S.
APPLICANT: Goddman, Warry S.
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2517
LEWITH G.78
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
FILE REFERENCE: 38-10(52052)8
FUNDERT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 6/360,039
PRIOR FILING DATE: 2002-02-21
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1.5%; Score 16; DB 6; Length 659;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.5%; Score 16; DB 6; Length 678; 100.0%; Pred. No. 6.4e-07; tive 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2518
LENGTH: 659
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                                                                                                                           ; TYPE: PRT; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-2518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT; ORGANISM: Schizosaccharomyces pombe US-10-369-493-2517
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; ORGANISM: Burkholderia fungorum
US-10-369-493-4874
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Best Local Similarity 100.(
Matches 16; Conservative
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SEQ ID NO 4874
LENGTH: 592
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)8 FILE REFERENCE: 38-10(52052)8 US/10/369, 493
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                                                                                                          GENERAL INFORMATION:
APPLICANT: NADLER, STEVEN G.
APPLICANT: CARMAN, JULIE
TITLE OF INVENTION: NF 'RB PATHWAY
FILE BEFERENCE: 3053-4191
CURRENT APPLICATION NUMBER: US/60/440,068
CURRENT APPLICATION NUMBER: 146
SOFTWARE: PATENT ON OS: 2.1
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TITLE OF INVENTION: Compositions and Methods for Halegenation Reactions
TITLE OF INVENTION: Compositions and Methods for Halegenation Reactions
TITLE OF INVENTION: Compositions and Methods for Halegenation Reactions
CURRENT APPLICATION NUMBER: US 6/10/148,907A
CURRENT FILING DATE: 2002-06-04
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 2000-01-03
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 23
LENGTH: 682
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100.0%; Pred. No. 0.0084;
Live 0; Mismatches 0; Indels
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. 0.0085;
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Pred. No.
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US-10-148-907A-23
; Sequence 23, Application US/10148907A
; GENERAL INFORMATION:
                                                                                         Sequence 572, Application US/60440068
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1.1%; Some Best Local Similarity 100.0%; P. Matches 12; Conservative 0;
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   CRGANISM: Homo sapiens US-60-440-068-572
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LENGTH: 677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 12; DB 6; 1
Pred. No. 0.0063;
0; Mismatches 0
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US-10-219-051B-12757
                                                                                                                                                                                                                                                         APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: HATOORI, WASHIRKI
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-02
PRIOR FILING DATE: 2001-06-03
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 44554
LENGTH: 504
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PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-08-14
PRIOR PILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/333,347
PRIOR FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 14715
SOFTWARE: Perl script
SEQ ID NO 12757
LENGTH: 676
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                                                                                                                              Sequence 14954, Application US/10156761 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Streptomyces avermitilis US-10-156-761-14954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.1%; Scc
Best Local Similarity 100.0%; Pi
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
SAPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
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US-10-219-051B-12757
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TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
FILE REPERBUES: BC1009 US DIVCIP
CURRENT APPLICATION NUMBER: US/10/188,523B
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US 09/627,216
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/147,719
PRIOR FILING DATE: 1999-08-06
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                                                          Length 691;
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_14776C.1.pep
US-10-424-599-191313
                                                        DB 6;
0.092;
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100.0%; Pred. No. 0.84;
tive 0; Mismatches (
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APPLICANT: HORIKAWA, JUNA
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: OSHIYUKI
TILE OF INVENITOR: NOVEL POLYNUCLEOTIDES
TITE OF INVENITOR: NOVEL POLYNUCLEOTIDES
CURRENT FILING DATE: 2002-05-29
PRIOR PELING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
SEQ ID NO 9867
LENGTH: 1352
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                                                        Score 11;
Pred. No.
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                                                      1.0%;
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Best Local Similarity 100.
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Sequence 187294, Application US/10424599

Sequence 187294, Application US/10424599

Sequence 187294, Application US/10424599

SEPERAL INFORMATION:
APPLICANT: La Rosa Thomas J

APPLICANT: Cao Vongwel

APPLICANT: Coo Vongwel

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 187294

LENGTH: 689
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GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Excyalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwel
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE OF INVENTION: NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 191313
LENGTH: 691
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US-10-424-599-187294
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0.0086;
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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Pred. No.
                PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 691
                                                                                                                   ; TYPE: PRT; ORGANISM: Saccharomyces cerevisiae US-10-369-493-22034
    2003-02-28
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Best Local Similarity 100.
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ORGANISM: Glycine max
FEATURE:
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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May 29, 2003, 08:37:32; Search time 99 Seconds (without alignments) 2181.186 Million cell updates/sec Run on:

US-10-031-146-2 1048 1 TIKEMPOPKTFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048 Title: Perfect score:

Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

671580 segs, 206047115 residues Searched:

0 Word size :

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SPTREMBL\_21:\* Database :

sp\_human: \*
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sp\_novertebrate: \*
sp\_mammal: \*
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sp\_plage: \*
sp\_plant: \*
sp\_rodent: \*
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sp\_vertebrate: \* sp\_unclassified:\* sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\* sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

					SUMMARIES	
Result		Query	:			
ON .	Score	Match	Match Length DB	<b>m</b> :	ID	Description
1	28	2.7	29	7	Q9AE23	Q9ae23 bacillus me
7	17	1.6	730	ო	Q8X1W0	Q8x1w0 coriolus ve
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4	14	1.3	069	ო	Q9HG14	Q9hq14 phanerochae
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9	13	1.2	558	m	094613	094613 schizosacch
7	13	1.2	597	4	090нв4	Q9uhb4 homo sapien
ω	13	1.2	597	4	Q96BC6	Q96bc6 homo sapien
6	13	1.2	605	16	032214	032214 bacillus su
10	13	1.2	209	16	Q9KF76	Q9kf76 bacillus ha
11	13	1.2	629	ო	Q9P4E1	Q9p4el cunninghame
12	13	1.2	671	ო	<b>Q9нFV</b> 3	Q9hfv3 rhizopus st
13	13	1.2	710	m	Q9P4E2	Q9p4e2 cunninghame
14	13	1.2	1066	m	Q9Y8G7	Q9y8q7 fusarium ox
15	12	1.1	527	16	Q9RD76	Q9rd76 streptomyce
16	12	1.1	969	11	QBR0Y3	Q8r0y3 mus musculu

096498 rhodotorula 096560 helianthus 043235 vicia sativ 034325 vicia sativ 034325 vicia sativ 038408 petroselinu 064349 petroselinu 064349 petroselinu 064349 petroselinu 064381 petroselinu 0642830 helianthus 096417 drosophila 09428 caenorhabdi 096561 helianthus 086562 micromonosp 086562 micromonosp 086562 micromonosp 086563 mays (m	70
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## ALIGNMENTS

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Yadav J.S., Loper J.C.;
"Cytochrome P450 oxidoreductase gene and its differentially terminated cobnas from the white rot fungus Phanerochaete chrysosporium.";
Curr. Genet. 37:65-73(2000).
EMBL; AF193062; AAG31351.1;
HSSP; P00388; LAMO.
InterPro; IPR00103997; FAD_binding.
InterPro; IPR001226; Flavodoxin_like.
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                                                                                                                                                                                                                                                                                                                                                                      Phanerochaete chrysosporium.
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Corticiaceae; Phanerochaete.
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Aphyllophorales; Corticiaceae; Phanerochaete.
NCBI_TaxID=5306;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNV-2002 (TrEMBLrel. 2), Last annotation update)
NADPH-dependent cytochrome P450 oxidoreductase (EC 1.6.2.4).
                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
NADPH-dependent cytochrome P450 oxidoreductase (EC 1.6.2.4)
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100.0%; Pred. No. 5.2e-05;
ive 0; Mismatches 0; Indels
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InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00656; FAD_binding; 1.
Pfam; PF00155; NAD_binding; 1.
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STRAIN-BKMF-1767;
MEDLINE-20136378; PubMed=10672447;
                              899 IMVGPGTGVAPFRGF 913
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PRINTS; PR00371; FPNCR.
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                                              Coriolus versicolor.
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Coriolus.
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Sukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus
NCBL_maxID=5061;
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van den Brink J., van Zeijl C., van den Hondel C., van Gorcom R.;
van den Brink J., van Zeijl C., van den Hondel C., van Gorcom R.;
"Cloning and characterization of the NADPH cytochrome P450
oxidoreductase (cpra) gene of Aspergillus niger.";
Submitted (ocr-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; Z26938; CAA891550.1;
HSSP; P16435; 1B1C.
                                                                                                                                                                                           Ichinose H., Wariishi H., Tanaka H.;
"Identification of cytochrome P450 oxidoreductase from white-rot
basidiomycete Coriolus versicolor.";
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                                                                                                                                                                                                                                                             Submitted (JUL-2011) to the EMBL/GenBank/DDBJ databases.
EMBL: AB063368; BAB83588.1; -
InterPro: PPR003097; FAD_binding.
InterPro: IPR001205; Flavdoxin_like.
InterPro: IPR001226; Flavdoxin_like.
InterPro: IPR001226; Flavdoxin_like.
InterPro: IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00667; FAD_binding; 1.
Pfam; PF00758; flavddoxin; 1.
Pfam; PF00758; flavddoxin; 1.
Pfam; PF00759; FLAVDOXIN.
PRINTS; PR00359; FLAVDOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.6%; Score 17; DB 3; Length 730;
100.0%; Pred. No. 4.2e-08;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.4%; Score 15; DB 3; Length 693; 100.0%; Pred. No. 4.8e-06; ... ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80742 MW; DB6FBC5FF3B15730 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            693 AA; 77072 MW; 1BEF35D4FC767674 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
NADPH cytochrome P450 oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            693 AA
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InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001226; Flavdoxin.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001403; Oxred_FAD_NAD(P).
Pfam; PF00667; FAD_binding; 1.
Pfam; PF00258; flavodoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
Cytochrome P450 oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   899 IMVGPGTGVAPFRGFVQ 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00175; NAD_binding; 1. PRINTS; PR00369; FLAVODOXIN. PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100. ses 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 730 AA;
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                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                     NCBI_TaxID=57466;
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Q00141;
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RESULT 3

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Homo sapiens (Human).
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Best Local Similarity
   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                              Q9UHB4;
Q9UHB4;
01-MAY-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                           Matches
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Q9UHB4
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PRINTS; PR00371; FPNCR.
Hypothetical protein; Oxidoreductase; Flavoprotein; FMN; FAD; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    542 NADP (RIBOSE PART) (BY SIMILARITY).
64199 MW; 12D64991612E7E00 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14; DB 3; Length 736;
Pred. No. 5.5e-05;
0; Mismatches 0; Indels
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
Putative NaDPH-cytochrome P450 reductase (EC 1.6.2.4).
SPAC1296.06
                                                                                                                                                                                                                                                                                                                                                                                                                  736 AA; 81627 MW; AC45F12C96198AB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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InterPro: IPR003097; FAD_binding.
InterPro: IPR001094; Flavodoxin_like.
InterPro: IPR001226; Flavodoxin.
InterPro: IPR001309; FPN_cyt_redctse.
InterPro: IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00567; FAD_binding; 1.
Pfam; PF00558; flavodoxin; 1.
Pfam; PF00755; NAD_binding; 1.
                                                                             InterPro; IPR003097; FAD_binding.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001226; Flavdoxin.
InterPro; IPR001709; FPN_CYL_redctse.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00265; FAD_binding; 1.
Pfam; PF00265; Flavdoxin; 1.
Pfam; PF00175; NAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pi
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NP_BIND 524 542 NAI
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EMBL; AF193061; AAG31350.1; -. EMBL; AF193060; AAG31349.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 902 GPGTGVAPFRGFVQ 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                           P00388: 1AMO
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MEDLINE-20092928; PubMed=10625700;
Paine M.J., Garner A.P., Powell D., Sibbald J., Sales M., Pratt N., Smith T., Tew D.G., Wolf C.R.;
Smith T., Tew D.G., Wolf C.R.;
Reductase.";
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1.2%; Score 13; DB 3; Length 558; 100.0%; Pred. No. 0.00046; Live 0; Mismatches 0; Indels
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015735; AAH15735.1; -.
InterPro; IPR003097; FAD_binding.
InterPro; IPR001226; Plavodoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     597 AA; 66762 MW; 0D1340D7280A4D8F CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
NADPH-dependent FWN and FAD containing oxidoreductase.
                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
NADPH-dependent FMN and FAD containing oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.2%; Score 13; DB 4; Le
100.0%; Pred. No. 0.00049;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                                               597 AA.
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InterPro; IPR001433; Oxred_FAD/NAD(P)
Pfam; PF00667; FAD binding; 1.
Pfam; PF001258; flavodoxin; 1.
Pfam; PF00175; NAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 275:1471-1478(2000).
EMBL; AF199509; AAF25205.1; -.
HSSP; P00388; IAMO.
InterPro; IPR003097; FAD_binding.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001226; Flavdoxin_like.
                                                                                                                                                                                                                                                  PRT;
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                                                                                                                   899 IMVGPGTGVAPFR 911
                                                13; Conservative
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InterPro; IPR001226; Flavodoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00667; FAD_binding; 1.
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Q9KF76;
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Q9P4E1;
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Q9P4E1
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                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of the gram-positive bacterium Bacillus subtilis.";
                                                         Gaps
                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Sulfite reductase [NADPH] flavoprotein alpha-component-like protein
                                                         ö
                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Bacillaceae; Bacillus.
NCBL_TaxID-1423;
                                         1.2%; Score 13; DB 4; Length 597;
100.0%; Pred. No. 0.00049;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Z99121; CAB15349-1; -.
HSSP: P003081; 1AMO.
    Pfam; PF00667; FAD_binding; 1.
Pfam; PF00258; flavodoxin; 1.
Pfam; PF00175; NAD_binding; 1.
SEQUENCE 597 AA; 66776 MW; E1C340CF93A95534 CRC64;
                                                                                                                      605 AA.
IPR001433; Oxred_FAD/NAD(P).
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InterPro; IPR001094; Flavdoxin_like.
                                                                                                                      PRT;
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454 IMVGPGTGVAPFR 466
                                                                     899 IMVGPGTGVAPFR 911
                                                       13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 390:249-256(1997)
                                                                                                                      PRELIMINARY;
                                                Similarity
                                                                                                                                                                             Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                               (YVGR protein).
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InterPro;
                                          Query Match
                                                 Local
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                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Bacillaces; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
NADPH-dependent cytochrome P450 oxidoreductase (EC 1.6.2.4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.2%; Score 13; DB 16; Length 607; 100.0%; Pred. No. 0.0005; ive 0; Mismatches 0; Indels
                                                                                                                                              Length 605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C-125 / JCM 9153;
MEDIINE-20512582; PubMed-11058132;
Bakani H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Ma
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                              Indels
                                                                                             605 AA; 67259 MW; 486F512COAED6217 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              607 AA; 67865 MW; 3CD1B0EAA1DBFFBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-077-2000 (TrEMBLrel. 15, Created)
01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-0UN-2002 (TrEMBLrel. 21, Last annotation update)
Sulfite reductase (NADPH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                           1.2%; Score 13; DB 16; L
100.0%; Pred. No. 0.0005;
1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    629 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                 607 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR001094; Flavdoxin_like.
Interpro; IPR001226; Flavodoxin.
Interpro: IPR001709; FPN_CYL_redctse.
Interpro; IPR001433; oxred_FAD/WAD(P).
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00667; FAD_binding; 1.
Pfam; PF00258; flavodoxin; 1.
Pfam; PF00258; flavodoxin; 1.
Pfam; PF00175; NAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00175; NAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
                                                                                                                                                                       100.08;
                                                                                                                                                                                                                                            899 IMVGPGTGVAPFR 911
                                                                                                                                                                                                                                                                          899 IMVGPGTGVAPFR 911
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Matches 13; Conservative
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus halodurans.
                                                                       Complete proteome. SEQUENCE 605 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 607 AA;
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                                                                                                                                                Query Match
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Gaps

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(Fragment)

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acid omega-
(EC 1.14.14.1);
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"Fusarium oxysporum fatty-acid subterminal hydroxylase (CYP505) is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20145435; PubMed=10679206; MEDLINE-20145435; Loper J.C.; Coloning and characterization of the cytochrome P450 oxidoreductase gene from the zygomycete fungus Cunninghamella."; Bliochem Blophys. Res. Commun. 268:345-353(2000). EMBL; AF195659; AAF89958.1; Bliochem Blophys. Res. Commun. 268:345-353(2000).
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Hypocreales; mitosporic Hypocreales; Fusarium.
NCBL_TaxID=5507;
                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2003 (TrEMBLrel. 2), Last annotation update)
NADPH-dependent cytochrome P450 oxidoreductase (EC 1.6.2.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.2%; Score 13; DB 3; Length 710;
100.0%; Pred. No. 0.00058;
ive 0; Mismatches 0; Indels
                                                       Indels
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Bifunctional P-450:NADPH-P450 reductase protein (Fatty hydroxylase) (P450foxy) [Includes: cytochrome P450 505
NADPH-cytochrome P450 reductase (EC 1.6.2.4)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     710 AA; 80021 MW; 8B3443AF5CDA3565 CRC64;
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Cunninghamellaceae; Cunninghamella.
            Pred. No. 0.00055;
                                                                                                                                                                                                                                                                                                                         710 AA.
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InterPro; IPR003097; FAD_binding.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001126; Flavdoxin.
InterPro; IPR001126; FPLavdoxin.
InterPro; IPR001143; Oxred_FAD/NAD(P).
Ffam; PF00258; FAD_binding; 1.
Ffam; PF00155; RAD_binding; 1.
Ffam; PF00175; NAD_binding; 1.
PKINTS; PR00369; FLAVODOXIN.
                                                                                                                                                                                                                                                                                                                      PRT;
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MEDLINE=20564350; PubMed=10995755;
100.08; Pr.
                                                                                                               902 GPGTGVAPFRGFV 914
                                                                                                                                              902 GPGTGVAPFRGFV 914
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Matches 13; Conservative
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Les 13; Conservative
                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cunninghamella elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4853;
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01-NOV-1999 (
01-NOV-1999 (
01-MAR-2002 (
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Q9P4E2;
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Matches
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Q9P4E2
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STRAIN—ATCC 26878;
MEDLINE=20145435; PubMed=10679206;
MEDLINE=20145435; DubMed=10679206;
Taday J.S., Loper J.C.;
"Cloning and characterization of the cytochrome P450 oxidoreductase gene from the zygomycete fungus Cunninghamella.";
Biochem. Biochys. Res. Commun. 268:345-353(2000).
HSSP; P16435; 1B1C.
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Kunic B., Truan G., Breskvar K., Pompon D.;
Finction cloning based on azole resistance in S. cerevisiae and characterization of R. nigricans redox carriers differentially involved in P450 dependent response to progesterone stress.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF290425; AAG23833.1; -.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
NADPH cytochrome P450 oxidoreductase iscenzyme 1 (EC 1.6.2.4).
Rhizopus stolonifer (Rhizopus nigricans).
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100.0%; Pred. No. 0.00052;
ive 0; Mismatches 0; Indels
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                                                                             Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
Cunninghamellaceae; Cunninghamella.
NCBI_TaxID=76405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
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InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001126; Flavdoxin.
InterPro; IPR001126; Flavdoxin.
InterPro; IPR001109; FPN_cyt_redctse.
InterPro; IPR001109; FPN_cyt_redctse.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF002667; FAD_binding; 1.
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00175; NAD_binding; 1.
PRINTS; PR00371; FPNCR.
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InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001026; Flavdoxin_like.
InterPro; IPR001709; FPM.cyt_redctse.
InterPro; IPR001403; Oxred_FAD/NAD(P).
Pfam; PP00667; FAD_binding; 1.
Pfam; PP00155; NAD_binding; 1.
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PRINTS; PR00371; FPNCR.
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                                                 Cunninghamella echinulata.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         629 AA;
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Les 13; Conserv
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SEQUENCE

Query Match

NON\_TER SEQUENCE

Query Match

Matches

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Q9HFV3; **Q9HFV3** 

RESULT 12 **09HFV3**  ö

Gaps

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STRAIN-A3(2);
Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                         SEQUENCE FROM N.A.
                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                              Nakayama N., Takemae A., Shoun H.;
"Cytochrome P450foxy, a catalytically self-sufficient fatty acid
hydroxylase of the fungus Fusarium oxysporum.";
-1. Blochem. 119:435-440(1996).
-1. FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. SHOWS HIGHEST
ACTIVITY TOWARD FATTY ACIDS WITH A CHAIN LENGTH OF 12-14 CARBONS
THE REDUCTASE DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
TO CYTOCHROME P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- COFACTOR: BINDS ONE MOLE EACH OF FAD AND FWN (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE: PROUSES: resu.
PROSITE: PSEGONG CYTOCHRONE_P450; 1.
Heme: Monooxygenase: Oxidoreductase; Membrane; Electron transport;
Homultifunctional enzyme; FMN; FAD; Flavoprotein; NADP.
DOMAIN 1 480 CYTOCHRONE P450.
DOMAIN 481 1066 NADPH-P-450 REDUCTASE.
BINDING 407 407 HEME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                 TO CYTOCHROME P450.

-I - CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + OXIDIZED FLAVOPROTEIN + H(2)0.

-I - CATALYTIC ACTIVITY: NADPH + 2 FERRICYTOCHROME = NADP(+) + 2
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0
membrane-bound eukaryotic counterpart of Bacillus megaterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.2%; Score 13; DB 3; Length 1066;
100.0%; Pred. No. 0.00085;
tive 0; Mismatches 0; Indels
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Saunders D.C., Harris D.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative cytochrome P450.
SCO0801 OR SCF43.12.
Streptomyces coelicolor.
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InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001226; Flavdoxin.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00667; FAD_binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001128; Cytochrome_P450.
                                              Biol. Chem. 275:39734-39740(2000)
                                                                                            FUNCTION, AND SUBCELLULAR LOCATION.
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                                                                                                                   STRAIN-MT-811;
MEDLINE-96271003; Pubmed-8830036;
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Pfam; PF00175; NAD_binding; 1.
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PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
PRINTS; PR00385; P450.
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Best Local Similarity
                       cytochrome P450BM3
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Pfam; PF00258
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                                             Redenbach M., Kleser H.M., Denapatte D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;

Kinashi H., Hopwood D.A.;

A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warrens T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete genome sequence of the model actinomycete Streptomyces
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PROSITE; PS00227; TUBULIN; 1.
Heme: Monocygenase; Oxidoreductase.
SEQUENCE 527 AA; 57741 MW; 4A612C1B7A894780 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coelicolor A3(2).";
Nature 417:141-147(2002).
-!- SIMILARIYY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; ALJ35502; CAB66201.1; -.
HSSP; P14779; 1BVY.
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100.0%; Pred. No. 0.0048;
lve 0; Mismatches 0;
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InterPro; IPR000217; Tubulin.
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STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
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Matches 12; Conservative
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PRINTS; PR00385; P450.
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May 29, 2003, 08:22:16; Search time 74 Seconds (without alignments) 1887.117 Million cell updates/sec
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5457
1 TIKEMPQPKTFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Amino acid sequenc	B. megaterium cyto	B. megaterium cyto	Amino acid sequenc	Amino acid sequenc	Amino acid sequenc	Bacillus megateriu	Amino acid sequenc	Amino acid sequenc	P450 17-alpha/P450
SUMMARIES		AAB46855	AAB46856	AAY93566	AAB31882	AAB31979	AAY72208	AAB31980	AAB31981	AAR11604
DB	22	22	22	21	22	22	22	22	22	12
Length	1048	1048	1048	1049	1049	1048	.1049	1048	1048	1085
å Query e Match Length DB	100.0	100.0	100.0	100.0	100.0	6.66	6.66	8.66	99.7	57.8
Score	5457	5457	5457	5457	5457	5450	5449	5444	5440	3154.5
Result No.	П	7	м	4	S	9	7	80	6	10

Schmid R;

Fischer M,

Schmitt J,

Schwaneberg U,

Hauer B, Pleiss J, Li Q; WPI; 2001-182800/18. N-PSDB; AAF54832.

Cytochrome P450 monooxygenase for oxidizing organic compounds, useful

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                                             The present sequence represents a cytochrome P450 monooxygenase. The specification describes a modified cytochrome P450 monooxygenase which can oxidize at least one of the following types of substrates: optionally substituted mono- or poly-cyclic aromatic heterocyclics containing nitrogen, sulphur or oxygen; optionally substituted mono- or poly-cyclic aromatics; linear or branched alkanes or alkenes; or optionally substituted cycloalkanes or cycloalkenes. The modified cytochrome P450 monooxygenase are specifically used to oxidize indole to indigo and indorubicin. However, they may be used to oxidize many
                                                                                                                                                                                                                                                                     1 TIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE
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especially for converting indole to indigo, has wide substrate range
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                      Claim 3; Page 35-39; 54pp; German.
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                                                                                                                                                          other substrates.
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This invention describes a novel electron donor system (M1) that
transfers electrons to an enzyme with redox properties comprising an
inorganic, not electrode-bound, electron sink and a mediator which enable
the electron transfer. The invention also describes (1) transferring (M2)
oxygen to a hydrocarbon containing hydrogen donor molecule, where the
hydrogen donor molecule is in a reaction medium comprising the oxygen
transferring enzyme and (M1) in the presence of oxygen and incubating
under suitable reaction conditions; (2) the enzymatic production (M3) of
terminally or subterminally hydroxylated (position omega-1 to omega-4)
centry acids comprising; (i) mixing a hydroxylatable fatty acid or fatty
acid derivative in the presence of (M1) and cytochrome P450
monooxygenase; and (ii) isolating the hydroxylated product; (3) a
conformation (2); and (4) detecting (M4) fatty acid-monooxygenases
comprising: (i) contacting the analyte with a omega-hydroxylatable fatty
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bioreactor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               le P450 monooxygenase; BM-3; electron donor system; bioreactor;
transfer; hydroxylatable fatty acid; fatty acid-monooxygenase.
              QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM
                                                                                                                                                                                   HTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADV
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10-MAR-2000; 2000DE-1011723.
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        label in (M1); and (ii) qualitatively or quantitatively detecting the signal. The invention is useful for the production of omega-hydroxylated fatty acids and the detection of fatty acid monoxygenases. The invention provides an alternative electron donor system of enzymes with redox properties that is cheaper and more efficient, where the enzyme
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 terminal chromophore or
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                                                                             HTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADV
                 VGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The specification describes a process for oxidizing an acyclic or cyclic terpene, a cycloalkene, or a derivative. The process comprises oxidizing the compound with a mutant haem-containing enzyme which comprises a substitution of an amino acid in the active site by an amino acid with a less polar side-chain. The process is useful for oxidizing an acyclic or cyclic terpene, a cycloalkene, or their derivatives. The process is also useful for product useful for preventing or treating infection in a human or animal body. The present sequence represents the amino acid sequence for use in the process of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TIKEMPQPRIFGELKNLPLLNTDRPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                              cycloalkene; haem-containing enzyme; mutant; oxidation;
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  P450-BM3 sequence
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Misc-difference 303
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of the
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  Amino acid sequence
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                                                                          infection; P450-BM3
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FDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNT 480
 Cytochrome P450 monooxygenase; oxidization; indole; indigo; indorubicin
                                                                                                                                                                                                                                                                         The present sequence represents a cytochrome P450 monooxygenase. The specification describes a modified cytochrome P450 monooxygenase which can oxidize at least one of the following types of substrates: optionally substituted mono- or poly-cyclic aromatic heterocyclics containing nitrogen, sulphur or oxygen; optionally substituted mono- or poly-cyclic aromatics; linear or branched alkanes or alkenes; or optionally substituted cycloalkanes or cycloalkenes. The modified cytochrome P450 monooxygenase are specifically used to oxidize indole to indigo and indorubicin. However, they may be used to oxidize many other substrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD
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has wide substrate
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                                                                                                                                                                      Schwaneberg U,
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                                                                                                      27-JUL-1999; 99DE-1035115.
18-NOV-1999; 99DE-1055605.
22-MAR-2000; 2000DE-1014085.
                                                                                   27-JUL-2000; 2000WO-EP07253
                                                                                                                                                                      Pleiss J,
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                       Bacillus megaterium
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                   KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD
                                                                       PVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDELMVLIPQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of a Bacillus P450 monooxygenase protein.
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            AFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL
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FDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGIPSPSTEOSAKKVRKKAENAHNT
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                                                                 GEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG
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                                                                                                                                                                        The present sequence represents a modified cytochrome P450 monooxygenase. The specification describes a modified cytochrome P450 monooxygenase which can oxidize at least one of the following types of substrates: optionally substituted mono- or poly-cyclic aromatic heterocyclics containing nitrogen, sulphur or oxygen; optionally substituted mono- or poly-cyclic aromatics; linear or branched alkanes or alkenes; or optionally substituted cycloalkanes or cycloalkenes. The modified cytochrome P450 monooxygenase are specifically used to oxidize indole to indigo and indorubicin. However, they may be used to oxidize indole other substrates.
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                                                                                                                                                                                                                                                                                                                                            this sequence does not appear in the specification; it was created information provided.
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has wide substrate
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   Fischer
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                                                                                         P450 monooxygenase for oxidizing for converting indole to indigo,
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Pred. No. 0;
   'n
     Schwaneberg
                                                                                         Cytochrome P450 monooxygenase
                                                                                                                                             Claim 5; Page -; 54pp; German.
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99.98;
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compounds. Also mutants of the monooxygenase enzyme with substitutions it the active site have enhanced oxidation activity. The process and the transgenic plant or animal which expresses the monooxygenase enzyme are used for detoxifying the environment polluted with the halo aromatic compounds. The present sequence is a Bacillus megaterium monooxygenase enzyme, P450BM-3, which is homologous to the monooxygenase
                                                                                                                                                                                                                                                                     DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRA
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99.8%;
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Best Local Similarity
Matches 1046; Conserv
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            QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM
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AFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL
                                                DASQQIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVEL
                                                                                              EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monooxygenase enzyme; P450BM-3 homologue; P450cam; oxidation; halogenated aromatic compound; electron transfer; putidaredoxin; putidaredoxin reductase; detoxification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        process for detoxifying environments contaminated with halo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aromatic compounds comprises treating the affected area with a monooxygenase enzyme -
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus megaterium monooxygenase enzyme homologue, P450BM-3.
                                                                                                                                                                                                                                                                                            HQVSEADARLWLQQLEEKGRYAKDVWAG 1048
                                                                                                                                                                                                                                                                                                        Disclosure; Page 32-39; 42pp; English.
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N-PSDB; AAD02365.
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                                                                                                                                                                                                                                           P450 monooxygenase; oxidization; indole; indigo; indorubicin.
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                      HTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADV
           VGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL
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                                              AAB31981 standard; Protein; 1048 AA.
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Best Local Similarity 99.7%;
Matches 1045; Conservative (
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 470 DGKLPSLEGHASLVLQIKPFKVKIEVRQ-----AWKEAQAEGSTPGTAENAHNTPLLV
                                                                                        LYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHPPDNA
                                                                                                                                                                           NVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGLDASQ
                                                                                                                                                                                         QIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALL
                                                  523 LYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHPPDNA
                                                                                                                                                                                                                                       TGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITLHTAF
                                                                           KQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEAD
                                                                                                                           ASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHGAFST
                                                                                                                                                                                                                                                                          EKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEKQASI
                                                                                                                                                                                                                                                                                                                           TVSVVSGEAWSGYGEYKGIASNYLAELOEGDTITCFISTPOSEFTLPKDPETPLIMVGPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome and NADPH-cytochrome p-450 reduction enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oxidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NADPH cytochrome p-450; reduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1025 EADARLWLQQLEEKGRYAKDVWAG 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1063 EADARLWL-QLEEKGRYAKDVWAG 1085
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waste.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85
                                                                                                                                                                                                                                                                                               The protein is a fusion of bovine adrenal cytochrome P450 17-alpha and Bacillus megaterium-derived cytochrome P450 BM-3. The fusion protein has the monoatomic oxygenation activity of the former and the reductivity supplying activity of the latter. Plasmid p(alphaBM1), containing the recombinant sequence encoding the fusion protein, is used to transform Saccharomyces creevisiae. The transformat is designated AH22(p(alphaBM-1)) and can be used for the synthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- DGLFTSWTHEKNWKKAHNILLPSFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEMPOPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKEAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YVGMVLNEALRLWPTAPAFSLY-AKEDTVLGGEYPLEKGDELMVLIPQLHRDKTIWGDDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QIIT ---FLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVL-VDPVPSYKQVKQLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DHINYELDIKETLILKPEGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNTPLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                       P450 reductase fused oxidase coding gene - has both mono-atomic oxygenation activity of bovine adrenal cytochrome p450 17-alpha and reductivity supplying activity
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12; Length 1085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YRDQPHPFITSMVRALDEAMNKLQRANPDDPAYDENKRQFQEDI-----
                           steroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                         adrenal;' cytochrome P450; oxidase; reductase;
1 p(alphaBM1).
                                                                                                                                                                                                                                                                                                                                                                                                                                    57.8%; Score 3154.5; DB 1;
60.9%; Pred. No. 1.2e-211;
iive 105; Mismatches 222;
P450 17-alpha/P450 BM-3 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DESRFDKNLSQALKFVRDFAG------
                                                                                                                                                                                                                                                                          8pp; Japanese,
                                                                                                                                     89JP-0197296
                                                                                                                                                              (SUMO ) SUMITOMO CHEM IND
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N-PSDB; AAQ11474.
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nes 672; Conserv
                                                                                                                                                                                                                                                                        Claim 1; Fig 2;
                                                             JP03061490-A.
                                                                                                              28-JUL-1989;
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	See also AAN81744-48.	δλ	8/9 CFISTPQSEFTLPKDPETP  :
	Sequence 1144 AA;	<b>අ</b> .	977 MFVRKSQFRLPFKSTTP
Quer; Best Matc}	Query Match 17.8%; Score 971.5; DB 9; Length 1144; Best Local Similarity 28.3%; Pred. No. 7.4e-59; Matches 320; Conservative 186; Mismatches 468; Indels 157; Gaps 43;	Qy Dp	
oy da	25 PVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKEACDESRFDKNLSQALKFVRDFAGD 84	QQ QQ	997 YICGDGSQMAPAVEATLMK:   :                     1094 YVCGDARNMAKDVQNTFYD
Oy Db	85 GLFTSWTHEKN	RESU AAP8 ID	RESULT 12 AAP81337 ID AAP81337 standard; protein;
Qγ	MMVDIAN:	XXX	
qa ,	HVSKEAEYLISKFQKIMAEVGHFDFFKYLVVSVANVICAICFGRRYDHDDQELLSIVN	БX	19-OCT-1990 (first entry)
참 점	1// MVRALDEAMNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKA 225 :	XX X	Expression prod. of plasmid   Cytochrome p450; NADPH cytoch
Oy Dp	226 SGEQSDDLLTHMLNGK-DPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALY 278 :	X X X	industrial Waste. JP63044888-A.
oy B	279 FLVKNPHVLQKAAEEAARVL-VDPVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYA 335 	NX P	25-FEB-1988. 12-AUG-1986; 86JP-0187713.
oy da	KEDTVLGGEYPLEKGDELMVLIPQLHRDKTIMGDDVEEFRPERPESTANSSYY, FIFTHST 	X X X X	12-AUG-1986; 86JP-0187713. (AGEN ) AGENCY OF IND SCI TE
	-FGNGQRACIGQQFALHEATLVLGMMLKHFDFEDHTNYELDIKETLTLKPEGFVV	R R X	WPI; 1988-094816/14. N-PSDB; AAN81746.
a ko	433 LFGLGRENCIGETIGRLEVFLFLAILLLQQMEFNVSPGEKVDMTPAYGLTLKHARCEHFQV 512 447 KAKSKKIPLGGIPSPSTEGS-AKKVRKRAENAHNTPLLVLYGSNMGTAEGTARDLADI 503	PT XX	Chimera fusion enzyme gene - and NADPH-cytochrome p-450 r
qq	: :	S X S	Disclosure; ; p; Japanese.
Oy Db	504 AMSKGFAPQVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKQFVDWLDQASA 556	3 <b>x</b> 8	See also AAN81/43-85 and AAN Seguence 1150 AA;
Š Š		On Was	Query Match 17.7%; Best Local Similarity 28.1%; Matches 320; Conservative 18
λ λ		δλ	25 PVQALMKIADELGEIFKFE
qq	GEMGRLKSYENOK	<b>a</b>	
Oy Dp	660GAFSTNVVASKELQQPGSARSTRHLEIEL-PKEASYQEGDHLGVIPRNYEGIVN 712 	ko qa	85 GLFTSWTHEKN  :    111 PDLYSFTLIANGQSWTFNP
Oy G	RVTAREG - LDASQOIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDEVTRTQLRAMAAK ::	Qy	118 MMVDIAVQLVQKWERLNAD :    :::   : 166 HVSKEAEYLISKFQKLMAE
, y	TVCPPHKVELBALLEKQAYKEQVLAKRITMLELLEKYPACEMKFSEFIALLPSI	δ 6	177 MVRALDEAMNK: :
<b>q</b> 0 :5	YASEPSEQEHLHKMASSSGEGKELYLSWVVEARRHILAILQDYPSLRPPIDHLCELLPRL	δδ	
e c	825 KPKYYELSSSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYL-AELQEGDYIT 878 	qq	:  : : :   376 TFEKGHIRDITDSLIEHCQI
		ا 0y	279 FLVKNPHVLQKAAEEAARV

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Score 968.5; DB 9; Length 1150;
Pred. No. 1.2e-58;
86; Mismatches 468; Indels 163; Gaps 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----WKKAHNILLPSFSQQAMKGY------HA 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAPGRVTRYLSSQRLIKEACDESRFDKNLSQALKFVRDFAGD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - coding oxidation enzyme of cytochrome p-450 reduction enzyme
                                                                                                     chrome p-450; reduction; oxidation;
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                                                                                                                                                                                                1150 AA
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(AGEN ) AGENCY OF IND SCI TECH.

WPI; 1988-094816/14.

86JP-0187713. 86JP-0187713.

12-AUG-1986; 12-AUG-1986;

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                                                                                           Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome p-450 and NADPH-cytochrome p-450 reduction enzyme
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453 IFGLGKRKCIGETIGRLEVFLFLAILLQOMEFNVSPGEKVDMTPAYGLTLKHARCEHFQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 17.6%; Score 962.5; DB 9; Local Similarity 28.1%; Pred. No. 3.2e-58; es 319; Conservative 186; Mismatches 469;
                                                                                                                                                                                                                                                                                                                                                                    See also AAN81743 and AAN81745-48
                                                                                                                                                                                                                                                                   Disclosure; ; p; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1150 AA;
N-PSDB; AAN81744
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Best Local Si
Matches 319;
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118   MAYDIAYOLVOKWERLNAD-EHIEVPEDMTRLTLDTIGLCGENTRENSEYRDQPHPFITS 176	Qy         447 KAKSKKIPLGGIPSPSTEGSA	651 ADMPLAKMH	0.0   0.0	975 VQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWL :::::::::::::::::::::::::::::::::::
OY YEGIVURVTAREGLDASQOIRLEAEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQL 764  1  ::	SULT 14 281336 AAP81336 standard; protein; 1162 AA. AAP81336; 19-OCT-1990 (first entry) Expression prod. of plasmid paLP17. Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation; industrial waste.	PN JP63044888-A.  XX  XX  XX  XX  XX  XX  XX  12-AUG-1986; 86JP-0187713.  XX  XX  XX  XX  AGEN ) AGENCY OF IND SCI TECH.  XX  XX  XX  XX  XX  XX  XX  XX  XX	PT Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome p-450 PT and NADPH-cytochrome p-450 reduction enzyme PX XX CC See also AAN81745-48.  CC See also AAN81743-84 and AAN81746-48.  SQ Sequence 1162 AA; Query Match Best Local Similarity 27.2%; Pred. No. 5.3e-55; Best Local Similarity 27.2%; Pred. No. 5.3e-55;	25 PVG 25 PVG 63 PHI 85 GLI

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completed: No. 182 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226 SGEO-----SDDLLTHMLNGK-DPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALY 278
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                                                                                                                                                                                                                                                                                     Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome p-450 and NADPH-cytochrome p-450 reduction enzyme
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                                                                                                            oxidation;
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
16.6%; Score 906.5; DB 9; Length 1132;
Best Local Similarity 27.2%; Pred. No. 2.6e-54;
Matches 308; Conservative 187; Mismatches 464; Indels 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----WKKAHNILLPSFSQQAMKGY-----
                                                                                                          p450; NADPH cytochrome p-450; reduction; waste.
                    AAP81338 standard; protein; 1132 AA.
                                                                                   Expression prod. of Plasmid pALP4.
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                                                                                                                                                                                                                                AGEN ) AGENCY OF IND SCI TECH
                                                                                                                                                                                      86JP-0187713
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                                                                (first entry)
                                                                                                                                                                                                                                                                                                                       Disclosure; ; ; Japanese
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N-PSDB; AAN81747.
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                                                                                                          Cytochrome industrial
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                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                          AAP81338;
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                                       ADIAMSKGFAPQVATLDSH----AGNLPR--EGAVLIVTASY-NGHPPDNAKQFVDWLDQ
                                                                                                                  554 ASADEVKGVRYSVFGCGDKNWATTYQKVPA---FIDETLAAKGAENIADRGEADASDDFE
                                                                                                                                                PSIRPRYYSISSSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYL-AELQEGDT----
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                                                                         SKDAHRYGIRGMSADPEEYDLADLSSLPEIDKSLVVFCMATYGEGDPTDNAQDFYDWLQE
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                                                                                                                                                                                              GTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMH-
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arch completed: May 29, 2003, 08:28:33
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May 29, 2003, 08:22:12 ; Search time 18 Seconds (without alignments) 1713.068 Million cell updates/sec
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5457
1 TIKEMPQPKTFGELKNLPLL......RLWLQQLEEKGRYAKDVWAG 1048
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Description	; ,	Sequence 14, Appr	Segmence 13. Appl	11	13,	4	'n	4	7	Sequence 4, Appli	4	21,	19,	Н	3,	9	'n	Ŋ	12,	Sequence 2, Appli	~	12,	7	7	7	7	Sequence 2, Appli
SUMMARIES	116-00-627-2168-14	IIS-07-642-002-2	90	80-	-08	US-08-705-625-4	US-09-010-998-5	US-09-220-574-4	US-08-365-486A-21	US-09-123-708-4	US-09-123-624-4	US-08-880-342-21	US-08-365-486A-19	US-08-880-342-19	US-08-705-625-3	US-09-010-998-6	US-09-220-574-3	US-08-147-812-5	US-08-319-866-12	US-09-123-708-2	US-09-123-624-2	US09-126-109-12	US-08-553-279-2	US-08-314-917-2	US-08-265-046-2	US-08-465-522-2	PCT-US93-11401-2
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2, 1	Sequence b, Appli Sequence 2, Appli Sequence 83, Appl Sequence 84, Appl	₹ K .	Sequence 98, Appl Sequence 99, Appl Sequence 25, Appl	Sequence 25, Appl Sequence 2, Appl1 Sequence 97, Appl	Sequence 102, App Sequence 96, Appl
PCT-US95-07849-2 US-08-319-866-10 US-09-123-708-6	US-U9-123-524-5 US-07-908-245-2 US-09-302-620B-83 US-09-302-620B-84	US-09-134-001C-4394 US-08-319-866-9 US-08-948-564-16	US-09-302-620B-98 US-09-302-620B-99 US-08-457-274A-25	PCT-US95-05758-25 US-09-144-367-2 US-09-302-620B-97	US-09-302-620B-102 US-09-302-620B-96
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## ALIGNMENTS

	19;	557	612 124	655 179	711	764	820
	Gaps	499 DLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKQFVDWLDQASAD	EVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDDFEGT :	613 YEEWREHMWSDVAAYFNLDIENSEDNKSTLSL	656 AKMHGAFSTNVVASKELQQPGSARSTRHLEIELPKEA-SYQEGDHLGVIPRNYEGIV 711	712 NRVTARFGLDASQQIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQL 764 1	765 RAMAAKTVCPPHKVELEALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFI-AL 820  :
Acid	588;	DEVDWE: 1 1 REYKWE	SEADAS     SLGDDD	-QFVDS.   :: OTFSEN	LGVIPR:     	VELQDP	CEMKFS1 :
	Length	PPDNAK        PTDNAA	ENIADR : KRFVPV	/FHDKP	OEGDH:  :     retgdh	SELLQY:	LEKYPA(
ion US/09627216A  ii, Sima F  ao-Song  Wei  Anthony  Bioproduction of para-Hydroxycinnamic  09 US NA  NUMBER: US/09/627,216A  2000-07-27  1999-08-06  3: 14  Office 97		SY-NGHI	AAKGAI :   :TEQGAI	PEYRV	KEA-S)	AKTVSVI	TMLEL
Hydro)	Query Match 12.9%; Score 705.5; DB 4; Best Local Similarity 31.9%; Pred. No. 2.1e-53; Matches 189; Conservative 92; Mismatches 245;	LIVTAS  -     FFFLAT	FIDETI :     VVDEGI	TLSI   :: PYTAA]	LEIELE    :: LEFDIS	PLA      LOPPFI	VLAKRI
para-	705.5 No. 2 smatch	PREGAV :1 KKETFA	rokvpa :  : ?nkial	NKS : : OKTAAT	ARSTRH      ORSCTH	fL    -  -	JAYKEQ 
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S/0962 mma F ng d cony colocti ony NA R: US, 0-07-2	. 98 9. 18 9. 19 7.	VATLDS   : -ADDEE	FGCGDF     :  FGLGNF	YFNLDI 	VASKEI     AVKKEI	IRLEAE   : FSLHII	ELEALI  :
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-216A-14  e 14, Application US/09 NO. 6368837  INFORMATION: ANT: Sariaslani, Sima F ANT: Tang, Xiao-Song ANT: Vannelli, Todd ANT: Vannelli, Todd ANT: Vannelli, Todd ANT: Gatenby, Anthony OF INVENTION: Bioproduc EFERENCE: BC1009 US NA. T APPLICATION NUMBER: U T FILING DATE: 1999-08-06 FILING DA	larit) Conse	DIAMSF       DYA	GV       GVWLE	WREHMV  : :  WKELVV	НGA 	TARFGI    EKLIGI	AAKTVC 
6A-14 4, Ap 6, Ap	th   Simi 189;	99 DLA 	558 EVK :   66 DDK	13 YEE : 15 FSA	6 AKM : 10 HTV	2 NRV	55 RAM   1:
SULT 1  -09-627-216A-14  Sequence 14, Application US/09627216A  Sequence 14, Application US/09627216A  Sequence 10, 3636837  APPLICANT: Sariaslant, Sima F  APPLICANT: Sariaslant, Sima F  APPLICANT: Tang, Xiao-Song  APPLICANT: Q1, Wei Wei  APPLICANT: Vannelli, Todd  APPLICANT: One Wei  APPLICANT: Gatenby, Anthony  TITLE OF INVENTION: Bioproduction of para-  TITLE OF INVENTION: Bioproduction of para-  CURRENT APPLICATION NUMBER: US/09/627,216A  CURRENT FILING DATE: 1999-08-06  NUMBER OF SEQ ID NOS: 14  SOFTWARE: Microsoft Office 97  SEQ ID NO 14  LENGTH: 588  TYPE: PRT  ORGANISM: Helianthus tuberosus  -09-627-216A-14	y Matc Local	24.5	ž, o	61	65	7.1	76
RESULT 1  US-09-627-216A-14  Sequence 14, Application US/0962; Patent No. 6568837  GENERAL INFORMATION: APPLICANT: Sariaslani, Sima F APPLICANT: Tang, Xiao-Song APPLICANT: Qi, Wei Wei APPLICANT: Qi, Wei Wei APPLICANT: Qi, Wei Wei APPLICANT: Gatenby, Anthony TITLE OF INVENTION: Bioproductis FILE REFERENCE: BC1009 US NA CURRENT APPLICATION NUMBER: US/; FURRENT FILING DATE: 1999-08-06 NUMBER OF SEQ ID NOS: 14  SEQ ID NO 14  LENGTH: 588  LENGTH: 588  TYPE: PRT  TYPE: PRT  CORRANISM: Helianthus tuberosus US-09-627-216A-14	Quer Best Matc	QY Db	oy Oy	č d	S G	QY Db	ò
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954 NNSLISNDRSWKRNKFRLTYVAEAPDLTQGLSNVHKKRVSAARLLSRQNLQSPKFSRSTI 1013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           638 NKSTLS-----LQFVDSAADMP--LAKMH--GAFSTNVVASKELQQPGSARSTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Bishopric, Nanette H.
AUNBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS: 31
ADDRESSE: ADDRESS:
ADDRESSE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
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CLASSIFICATION: 514
ATTONREY/ACENT INFORMATION:
NAME: Sholtz, Charles K.
REGIETRATION NUMBER: 38 615
REFRENCE/DOCKET NUMBER: 8255-
TELECOMMUNICATION INFORMATION:
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LALAAHASDATEADRLQFLASREGKDEYAEWIVANQRSLLEVMEAFPSAKPPLGVFFAAI 359
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                                        LPSIRPRYYSISSSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNY-----LAELQEG
                                                                               360 APRLQPRYYSISSSPKMVPNRIHVTCALVY-EKTPGGRIHKGICSTWMKNAVPLTENQDC
                                                                                                                                                                                                                                            GCRNRKVDFIYENELNNFVENGALSELDMAFSR-EGASKEYVQHKMSQKASDIWNMLSEG
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                                                                                                                      DTITCFISTPQSEFTLPKDPBTPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYF
                                                                                                                                                                                                      GCRSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQG
                                                                                                                                                                                                                                                                                     994 AHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVW 1046
                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Bredt, David S.
APPLICANT: Hang, Paul M.
APPLICANT: Reed, Randall
APPLICANT: Snyder, Solomon H.
TITLE OF INVENTION: Purification and Molecular Cloning of Nitric
TITLE OF INVENTION: Oxide Synthase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Banner, Birch, McKie & Beckett
STREET: One Thomas Circle, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.4%; Score 678; DB 1; Length 1429; ilarity 28.2%; Pred. No. 2.6e-50; Conservative 126; Mismatches 265; Indels 10
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MEDIUM TYPE: RIORPY disk
COMPUTER: BAPPY disk
COMPUTER: BAPP C COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.24
CURRENT APPLICATION NUMBER: US/07/642,002
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/07642002
Patent No. 5268465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION UNDRER: 32,141
REFERENCE/DOCKET NUMBER: 1107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 296-5500
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 193; Conserv
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKSTLS------LQFVDSAADMP--LAKMH--GAFSTNVVASKELQQPGSARSTR 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    683 HLEIEL--PKEASYQEGDHLGVIPRNYEGIVNRVTARF--GLDASQQIRLEAEEEKLAHL 738
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                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                   Query Match
12.4%; Score 678; DB 2; Length 1429;
Best Local Similarity 28.2%; Pred. No. 2.6e-50;
Matches. 193; Conservative 126; Mismatches 265; Indels 100;
                                                                                                                                                                                                                                                                                                                                    505 MSKGFAPQVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKQF----
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APPLICANT: Yin, Jerry C.
APPLICANT: Regulski, Michael
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES
TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSEADARLWLQQLEEKGRYAKDVW 1046
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LSEEDAGVFISRLRDDNRYHEDIF 1395
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TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1429 amino acids
                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-365-486A-13
                                                                                              amino acid
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954 NNSLISNDRSWKRNKFRLTYVAEAPDLTQGLSNVHKKRVSAARLLSRQNLQSPKFSRSTI 1013
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                     3: Hamilton, Brook, Smith & Reynolds, P.C. Two Militia Drive
                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.4%; Score 678; DB 2; Best Local Similarity 28.2%; Pred. No. 2.6e-50; Matches 193; Conservative 126; Mismatches 265
                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,866
FILING DATE: 7-OCT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: CST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1429 amino acids
CORRESPONDENCE ADDRESS:
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                                                                                                    Massachusetts
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid STRANDEDNESS:
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                                                                         Lexington
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                     ADDRESSEE:
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                                                                                                                             COUNTRY:
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505 778 548 838 583 638	954 NNSLISNDRSWKRNKFRITTYVAEAPLTOGESNVHKKRVSARELISRONLÖSPKESKSTI 683 HEBIEL-PERASYQEGDHLGVIPRNYGARFGLDASQULEBAEBEKLAHL : :	1313 SREPDRPKKYVQDVLQEQLAESVYRALKEGGGHIYVCGD 1023 VSEADARLWLQQLEEKGRYAKDVW 1046 1171       :::         :::   1372 LSEEDAGVFISRLRDDNRYHEDIF 1395  SULT 6 -08-705-625-4 Sequence 4, Application US/08705625 Retent No. 5008756 GENERAL INFORMATION: APPLICANT: Samie R. APPLICANT: Jaffrey, Samie R. APPLICANT: Jaffrey, Samie R. APPLICANT: Jaffrey, Samie R. TITLE OF INVENTION: Oxide Synthase NUMBER OF SQUENCES: 16 CORRESPONDENCE ADDRESS: ADDRESSEE: Banner & Witcoff STREET: 1001 G Street, N.W. CITY: Washington, D.C. CONPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: COMPU	H
\text{\tint{\text{\tin}\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\tex{\tex	4 5 4 5 4 5 4 5 4 5	4 4 4 4 8 8 4 4 4 4 4 4 4 4 4 4 4 4 4 4	
1194	RESULT 5 US-08-880-342-13 ; Sequence 13, Application US/08880342 ; Patent No. 6218179 ; GENERAL INFORMATION:     APPLICANT: Bushopric, Nanette H.     APPLICANT: Murphy, Brian     APPLICANT: Murphy, Brian     APPLICANT: Application Tissue Specific Hypoxia Regulated     TITLE OF INVENTION: Tissue Specific Hypoxia Regulated     TITLE OF INVENTION: Tissue Specific Constructs     NUMBER OF SEQUENCES: 37     CORRESPONDENCE ADDRESS:     STREET: 350 Cambridge Avenue, Suite 250     CITY: Palo Alto     STREET: CA     COUNTRY: USA     ZIP: 94306     COUNTRY: IBM PC Compatible	ING SYSTEM: PC-DOS/MS-DOS RE: Patentin Release #1.0, Version #1.2 APPLICATION DATA: ATION NUMBER: US/08/880,342 DATE: 23-UUN-1997 PLICATION DATA: ATION NUMBER: PCT/IB95/00996 PLICATION DATA: ATION NUMBER: PCT/IB95/00996 PLICATION DATA: ATION NUMBER: DS 08/365,486 DATE: 13-NOV-1994 AGENT INFORMATION: Sholtz, Charles K. RATION NUMBER: 38,615 RATION NUMBER: 38,615 SHOLZ, Charles K. RATION NUMBER: 38,615 SHOLZ, CHARLES K. RATION NUMBER: 38,615 CHARATERISTICS: 11429 amino acids TYPE: protein	Query Match  12.4%; Score 678; DB 4; Length 1429;  Best Local Similarity 28.2%; Pred. No. 2.6e-50;  Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;  Qy 457 GIPSPSTEQSAKKVRKAENAHNTPLLVLYGSNMGTAEGTARDLADIA 504  Db 718 GINGTPTKRAIGFKKLAEAVKFSAKLMGQAMAKRVKATILYATETGKSQAYAKTLCEIF 777

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SRMPNOPKTYVQHVMEQDGKKLI--ELLDQGAHFYICGDGSQMAPAVEATLMKSYADVHQ 1022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 739 PLAKTVSVEELL-----QYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE-KQ 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- LQFVDSAADMP--LAKMH--GAFSTNVVASKELQQPGSARSTR 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLEIEL---PKEASYQEGDHLGVIPRNYEGIVNRVTARF--GLDASQQIRLEAEEEKLAHL 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEKQASITVS 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVSGEAWSGYGE-YKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIMVGPGTG 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAPFRGFVQARK-QLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGII-TLHTAF 964
                                                                                                                                                                                                                                                                                                                                   457 GIPSPSTEQSAKKVRKKAE------NAHNTPLLVLYGSNMGTAEGTARDLADIA 504
                                                                                                                                                                                                                                                                                                                                                        -----VDWLDQ-ASADEVKGVRYSVFGCGDKNWATTYQKVP 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKSYKVRFNSVSSYSDSRKSSGDGPDLRDNFESTGPLANVRFSVFGLGSR----AYPHFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF---IDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFNL--DIENSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.4%; Score 678; DB 2; Length 1430;
Best Local Similarity 28.2%; Pred. No. 2.6e-50;
Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    505 MSKGFAPQVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKQF-----
               01107.57071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|| || ::::| : || :|::
1372 LSEEDAGVFISRLRDDNRYHEDIF 1395
            REFERENCE/DOCKET NUMBER: 0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-929
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1430 amino acids
REGISTRATION NUMBER: 32,141
                                                                                                                                                                                                              ; ORGANISM: Homo sapiens US-08-705-625-4
                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                   amino acid
                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          788
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Sequence 5, Application US/09010998 Patent No. 6103872

RESULT 7 US-09-010-998-5

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954 NNSLISNDRSWKRNKFRLTYVAEAPDLTQGLSNVHKKRVSAARLLSRQNLQSPKFSRSTI 1013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        638 NKSTLS------LQFVDSAADMP--LAKMH--GAFSTNVVASKELQQPGSARSTR 682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :: : : | | ||:||:: | ||:| |:: | |-:: | |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: |-:: 
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                                                                                                             APPLICANT: Eliasson, Mikael
APPLICANT: Cohen, No. 6103872m
TITLE OF INVENTION: CAPON, a protein that binds
TITLE OF INVENTION: neuronal nitric oxide synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASIED for Windows Version 2.0
SOFTWARENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,998
FILING DATE: 22-AN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: No. 6103872e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1430 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
: Snyder, Solomon
                                       Jaffrey, Samie
Snowman, Adele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-508-9299
                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS: ADDRESSEE: Banner & V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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COUNTRY:
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1253 IAPFRSFWQQRQFDLQHKGMNPCPMVLVFGCRQSKIDHIYREETLQAKNKGVFRELYTAY 1312
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                                                                       894 AFGHAVDTLLEELGGERILKMREGDELCGQEEAFRTWAKKVFKAACDVFCVGDDVNIEKP 953
                                            -----NAHNTPLLVLYGSNMGTAEGTARDLADIA 504
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                                                                                                                                                                                                                                                             838 RKSYKVRFNSVSSYSDSRKSSGDGPDLRDNFESTGPLANVRFSVFGLGSR----AYPHFC
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                                                                                                                                                                                                                     ---VDWLDQ-ASADEVKGVRYSVFGCGDKNWATTYQKVP
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    Indels 100; Gaps
                                                                                                                                505 MSKGFAPQVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKQF----
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APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
    Mismatches 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 350 Cambridge Avenue, Suite 250 CITY: Palo Alto STATE: CA COUNTRY: - USA
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1372 LSEEDAGVFISRLRDDNRYHEDIF 1395
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  Conservative 126;
                                               GIPSPSTEQSAKKVRKKAE---
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ADDRESSEE: Dehlinger
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US-08-365-486A-21
    Matches 193;
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                                          1074 GVISNWKDESRLPPCTIFQAFKYYLDITTPPTPLQQQFASLATNEKEKQRLLVLSKGLQ 1133
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                                                                                                           788 AYKEQVLAKRLIMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEKQASITVS 847
                                                                                                                                                                      VVSGEAWSGYGE-YKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIMVGPGTG 906
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739 PLAKTVSVEELL------QYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE-KQ 787
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APPLICANT: Jaffrey, Sanie R.
APPLICANT: Jaffrey, Sanie R.
APPLICANT: Jaffrey, Sanie R.
APPLICANTION: Protein Inhibitor of Neuronal Nitric
TITLE OF INVENTION: Oxide Synthase
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
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Pred. No. 2.6e-50;
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REGISTRATION NUMBER: 32,141
REPERNICE/DOCKET NUMBER: 01107.57071
TELECOMMUNICATION:
TELECHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                   VSEADARLWLQQLEEKGRYAKDVW 1046
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1372 LSEEDAGVFISRLRDDNRYHEDIF 1395
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/705,625
FILING DATE: 30-AUG-1996
ATTORNEY/AGENT INFORMATION:
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; Sequence 4, Application US/09220574
; Patent No. 6168926
; GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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Cytomegalovirus
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US-09-123-708-4
US-09-123-708-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 675; DB 2; Length 1433;
Pred. No. 4.9e-50;
2; Mismatches 258; Indels 104;
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               APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REGISTRATION NUMBER: 38,615
REGISTRATION NUMBER: 38,615
RELECOMMUNICATION INFORMATION:
TELEPONE: (415) 324-0960
INFORMATION FOR: SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1433 amino acids
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1374 GKLSAEDAGVFISRMRDDNRYHEDIF 1399
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12.4%; Sco
Best Local Similarity 28.0%; Pro
Matches 192; Conservative 132;
CURRENT APPLICATION DATA:
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957 ANNSLISNDRSWKRNKFRLTFVAEAPELTQGLSNVHKKRVSAARLLSRQNLQSPKSSRST 1016
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                                                                                                                         GENERAL INFORMATION:
APPLICANT: SCHRADER, JUEFGEN
APPLICANT: SCHRADER, JUEFGEN
APPLICANT: GOEDECKE, Axel
TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
FILE REFERENCE: 511169-2003
CURRENT APPLICATION NUMBER: US/09/123,708
CURRENT FILING DATE: 1996-03-01
EARLIER APPLICATION NUMBER: 08/553,503
EARLIER PILING DATE: 1996-03-01
EARLIER PELING DATE: 1996-03-01
EARLIER PILING DATE: 1994-03-31
NUMBER OF SEQ ID NOS: 6
SOFTHARE: PATENTIN VAF. 2.0
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Sequence 4, Application US/09123708
Patent No. 6146887
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1315 AYSREPDKPKKYVQDILQEQLAESVYRALKEQGGHIYVCGDVTMAADVLKA-IQRIMTQQ 1373
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                                                                                                                                                                                                    Sequence 4, Application US/09123624

Patent No. 6149936

GENERAL INFORMATION

APPLICANT: SCHRADER, Jurgen

APPLICANT: GODECKE, Axel

TITLE OF INVENTION: DNB EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC

TITLE OF INVENTION: DNB EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC

TITLE OF INVENTION: DATE: 1998-01-28

CURRENT PILICATION NUMBER: 08/09/123,624

CURRENT FILING DATE: 1998-03-01

PRIOR FILING DATE: 1998-03-01

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PATENTIN VET: 2.1

SOFTWARE: PATENTIN VET: 2.1

SOFTWARE: PATENTIN VET: 2.1
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TGIAPFRSFWQQRQFDIQHKGMNPCPMVLVFGCRQSKIDHIYREETLQAKNKGVFRELYT 1314
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1374 GKLSAEDAGVFISRMRDDNRYHEDIF 1399
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ORGANISM: Homo sapiens
US-09-123-624-4
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Best Local Similarity
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722 GINGIPIKRRAIGFKKLAEAVKFSAKLMGQAMAKRVKATILYATETGKSQAYAKTLCEI- 780
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                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Tissue Specific Hypoxia Regulated TITLE OF INVENTION: Therapeutic Constructs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 4;
4.9e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
1021 HQVSEADARLWLQQLEEKGRYAKDVW 1046
                                         1374 GKLSAEDAGVFISRMRDDNRYHEDIF 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                Sequence 21, Application US/08880342
Patent No. 6218179
                                                                                                                                                                                                                                  APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger
STREET: 350 Cambridg
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
SOFTWARE: PatentI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Pa]
STATE: CA
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23; 504 781 547 841 581 897 636 957 681

Gaps

us-10-031-146-2\_1.rai

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1077 ALGVISNWTDELRLPPCTIFQAFKYYLDITTPPTPLQLQQFASLATSEKEKQRLLVLSKG 1136
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                                                                                                                                                                                                                                                                                                                                                                 457 GIPSPSTEQSAKKVRKKAE------NAHNTPLLVLYGSNMGTAEGTARDLADIA
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                                                                                                                                                                                                                                                                                 Indels 104;
                                                                                                                                                                                                 Length 1434;
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APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
                                                                                                                                                                                                 Score 675; DB 2; I
Pred. No. 4.9e-50;
2; Mismatches 258;
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ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/08880342
Patent No. 6218179
                                                                                                                                                                                                     Query Match 12.4%; So
Best Local Similarity 28.0%; Pr
Matches 192; Conservative 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Webster, Keith A
                                                                           MOLECULE TYPE: protein
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    amino acid
                                          linear
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APPLICANT: Webster
                                                                                    ; MOLECULE TYP;
US-08-365-486A-19
                                          TOPOLOGY:
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US-08-880-342-19
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582 PAF---IDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFNL--DIENSE 636
                                                                                                                                                                                                                                                                                                                   682 RHLEIEL--PKEASYQEGDHLGVIPRNYEGIVNRVTARFGLDA---SQQIRLEAEEEK-- 734
                                                                           CAFGHAVDTLLEELGGERILKMREGDELCGQEEAFRTWAKKVFKAACDVFCVGDDVNIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      786 KQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEKQASIT
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                                                                                                                                                       DNKSTLS------LQFVDSAADMP--LAKMH--GAFSTNVVASKELQQPGSARST
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APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1021 HQVSEADARLWLQQLEEKGRYAKDVW 1046
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1374 GKLSAEDAGVFISRMRDDNRYHEDIF 1399
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23-DEC-1994
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NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/POCKET NUMBER: 82;
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Palo Alto
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                                                                                                                                              905 TGVAPFRGFVQARK-QLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGII-TLHT 962
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                                                                    457 GIPSPSTEQSAKKVRKKAE-----NAHNTPLLVLYGSNMGTAEGTARDLADIA
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                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Snyder, Solomon n. APPLICANT: Snyder, Solomon n. APPLICANT: Jaffrey, Samte R. TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric TITLE OF INVENTION: Oxide Synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.4%; Score 675; DB 2; 28.0%; Pred. No. 5.6e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 12.4%; Score 675; DB Best Local Similarity 28.0%; Pred. No. 5.6e-Matches 192; Conservative 132; Mismatches
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                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08705625 Patent No. 5908756 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 30-AUG-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Banner & Witcoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1001 G Street, N.W. CITY: Washington, D.C. COUNTRY: U.S.A. ZIP: 20001-4597
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TITLE OF INVENTION: OXIG
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Wi
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                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 132; Mismatches
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Sholtz, Charles K.
RECISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.4%; Score 675; 28.0%; Pred. No. 4
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APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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amino acid
                                                                                                  COMPUTER READABLE FORM:
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Best Local Similarity
Matches 192; Conserv
                    Palo Alto
                                                                                                                                                                                                                                            FILING DATE: 23
CLASSIFICATION:
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582 P	637 D 958 A	682 R	735 - 1077 A	786 K	846 V 1 1197 V	905 T 1 1256 T	963 A 1 1316 A	1021 H 1375 G
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Search completed: May 29, 2003, 08:22:44 Job time : 24 secs

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May 29, 2003, 08:22:16; Search time 30 Seconds (without alignments) 3536.081 Million cell updates/sec
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Maximum DB seq length: 2000000000
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Published\_Applications\_AA:\*

Database :

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Sequence 14, App Sequence 14, Appl Sequence 23, Appl Sequence 124, App Sequence 13, Appl Sequence 118, Description Sequence 1 Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seguence Sequence Sequence US-10-138-838-117 US-10-139-031-117 US-10-139-031-118 % Query Match Length DB Score Result ٠ ي

23;

Gaps

64;

Length 677;

Query Match 14.0%; Score 766; DB 9; Length 677; Best Local Similarity 32.4%; Pred. No. 8.1e-48; Matches 211; Conservative 113; Mismatches 264; Indels

ORGANISM: Homo sapiens US-09-371-347-23

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9 US-10-138-905-118	9 US-10-138-916-118	9 US-09-976-800-118	10 US-09-911-781-11	9 US-10-138-838-84	9 US-10-139-031-84	9 US-10-138-905-84	9 US-10-138-916-84	9 US-09-976-800-84	9 US-09-371-347-44	9 US-09-371-347-2	9 US-09-371-347-21	9 US-09-371-347-42	9 US-09-371-347-46	9 US-09-778-319-2	9 US-09-371-347-22	_	_	9 US-10-063-547-54	9 US-09-989-735-264	ns	9 US-09-989-730-264	nS	9 US-09-991-181-264	9 US-09-993-687-264	9 US-09-989-734-264
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## Squence 23, Application US/09371347 Fublication No. US20030082676A1 GENERAL INFORMATION: APPLICANT: ROY A. Gravel et al. TITLE OF INVENTION: CLONING, AND METHODIS FOR EVALUATING RISK OF TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER TILL REFERENCE: 50004/003003 CURRENT APPLICATION NUMBER: 08/09/371,347 FRIOR FILING DATE: 1999-01-15 PRIOR APPLICATION NUMBER: 09/232,028 PRIOR PRIOR FILING DATE: 1999-01-15 NUMBER OF SEQ ID NOS: 51 SOFTWARE: FASTSEQ for Windows Version 4.0 US-09-371-347-23 LENGTH: 677 TYPE: PRT SEQ ID NO 23

ALIGNMENTS

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NAME/KEY: CHAIN
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TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
FILE REFERENCE: BC1009 US CIP
CURRENT APPLICATION NUMBER: US/09/765,873A
CURRENT FILING DATE: 2001-01-19
PRIOR PEDICATION NUMBER: US 60/147,719
PRIOR APPLICATION NUMBER: US 60/147,719
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 38
SOFTWARE: MICROSOft Office 97
SEQ ID NO 14
LENGTH: 588
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APPLICANT: Vogels, Ronald V.
APPLICANT: Vogels, Ronald V.
APPLICANT: Vogels, Refan F.F.
TITLE OF INVENTION: Gene thrrapy for enhancing and/or inducing anglogenesis
FILE REFERENCE: 2183-5233US
CURRENT APPLICATION NUMBER: US/10/224,249
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: PCT/NL00/00482
PRIOR PLING DATE: 2000-07-07
PRIOR FILING DATE: 1099-07-09
PRIOR FILING DATE: 1099-07-09
PRIOR FILING DATE: 1999-07-09
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712 NRVTARFGLDASQQIRLEAEEEKLAHL-----PLAKTVSVEELLQYVELQDPVTRTQL 764
                                                                                                                       EEAEKLIGLPADTYFSLHIDNEDGTPLGGPTLQPPFPPCTLRKALTNYADLLSSPKKSTL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                875 DTITCFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYF 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCRSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQG 993
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Best Local Similarity 28.0%; Pred. No. 1.2e-40;
Matches 192; Conservative 132; Mismatches 258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/10224249 Publication No. US20030087867A1 GENERAL INFORMATION:
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SEQ ID NO 14
LENGTH: 1433
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Sequence 13, Application US/10224249
Publication No. US20030087867A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Vogels, Ronald V.
APPLICANT: Vogels, Ronald V.
APPLICANT: Vorilnden, Stefan F.F.
FILE REPERBNCE: 2183-553340
CURRENT APPLICATION NUMBER: US/10/224,249
PRIOR APPLICATION NUMBER: PCT/NL00/00482
PRIOR APPLICATION NUMBER: FCT/NL00/00482
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: EP 99202263.2
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                                                                                                                       KLIELL--DQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYA 1042
 --KLAHLPLAKTVSVEEL 749
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                                                                                                                                                                  SINVPAAFLLSQLPILKPRYXSISSSQDHTPSEVHLTVAVVTYRTRDGQGPLHHGVCSTW
                                                                                                                                                                                                                      LAELQEGDTITCFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGFVQAR-KQLKEQGQS
                                                                                                HIGIFPGNQTALVQGILERV-VDCPTPHQTVCLEVLDESGSYWVKDKRLP---PCSLSQA
                                                                                                                                               ACEMKFSEFIALLPSIRPRYSISSPRVDEKQASITVSVVSGEAWSGYGE-YKGIASNY
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                                                                         LQY - VELQDPVTRTQLRAMAAKTVCPPHKVELEALLEKQAYKEQVLAKRLTMLELLEKYP
                                                                                                                                                                                                                                                                                              LGEAHLYFGCRSPHEDYLYQEEL-ENAQSEGIITLHTAFSRMPNQPKTYVQHVME-QDGK
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COTHER INFORMATION: Homo sapiens inducible nitric oxide synthase US-10-224-249-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1153;
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 HLGVIPRNYEGIVNRVTARFGLDA - - - SQQIRLEAEEE -
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SOFTWARE: PatentIn version 3.1
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EDIF 1122
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APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOFLASTIC DISEASE
FILE REFERENCE: 87079/870,759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
SEQ ID NO 124
LENGTH: 1144
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                                                                                                                                                                                                                                         .076 ALGVISNWIDBELRLPPCTIFQAFKXYLDITTPPTPLQLQQFASLATSEKEKQRLLVLSKG 1135
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TGIAPFRSFWQQRQFDIQHKGMNPCPMVLVFGCRQSKIDHIYREFLQAKNKGVFRELYT
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                           957 ANNSLISNDRSWKRNKFRLTFVAEAPELTQGLSNVHKKRVSAARLLSRQNLQSPKSSRST
                                                                       RHLEIEL--PKEASYQEGDHLGVIPRNYEGIVNRVTARFGLDA---SQQIRLEAEEEK--
                                                                                                                                               -----LAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE-
                                                                                                                                                                                                                                                                                          VSVVSGEAWSGYGE-YKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIMVGPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            484 VLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSH-AGNLPREGAVLIVTASY-NGHPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA----KQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAF---IDETLAAKGAE
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                                                                                                                        555 SADEVKKVRYSVFGCGDKNWATTYQKVPAF---IDETLAAKGAENIADRGEADASDDFEG 611
                                                                                                                                                                                                                                                                                                                                                                    715 TARF--GLDASQQIRLEAEEEKLAHLPLAKTV---SVEELLQY-VELQDPVTRTQLRAMA 768
                                          497 ARDLADIAMSKGFAPQVATLDSH-AGNLPREGAVLIVTASY-NGHPPDNAKQFVDWLDQA 554
                                                                                                                                                                                                                                            668 AFRSWAVQTFKAACETFDVRGKQHIQIPKLYTSNVTWDPHHYRLVQDSQPLDLSKALSSM 727
                                                                                                                                                                                                                                                                                      659 H--GAFSTNVVASKELQQPGSARSTRHLEI--ELPKEASYQEGDHLGVIPRNYEGIVNRV 714
                                                                                                                                                   613 KELNNK-FRYAVFGLG----SSMYPRFCAFAHDIDQKLSHLGASQLTPMGEGDELSGQED
                                                                                554 AWDLGAL-FSCAFNPKVVCMDKYRLSCLEEERLLLVVTSTFGNGDCPGNGEKLKKSLFML
                                                                                                                                                                                                        TYEEWREHMWS-----DVAAYFNLDIENSEDNKSTLS---LQFVDSAADMPLAK----M
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SOFTWARE: Pater
SEQ ID NO 15
LENGTH: 1203
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APPLICANT: Galler, David A.
APPLICANT: Simmons, Richard K.
APPLICANT: Simmons, Richard K.
APPLICANT: Simmons, Richard K.
TITLE OF INVENTION: Inducible Nitric Oxide Synthase Gene for Treatment of TITLE OF INVENTION: Disease
CURRENT APPLICATION NUMBER: 08/09/992,056
CURRENT FILING DATE: 12984-10-21
PRIOR APPLICATION NUMBER: 09/176,496
PRIOR APPLICATION NUMBER: 09/176,496
PRIOR APPLICATION NUMBER: 08/465,522
PRIOR APPLICATION NUMBER: 08/465,522
PRIOR APPLICATION NUMBER: 08/314,917
PRIOR FILING DATE: 1994-09-28
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1992-11-25
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEMLEMAQKGVLHAVHTAYSRLPGKPKVYVQDILKQQLASEVLRVLHKEPGHLYVCGD-V 1085
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613 KELNNK-FRYAVFGLG----SSMYPRFCAFAHDIDQKLSHLGASQLTPMGEGDELSGQED 667
                                                                                                                      H--GAFSTNVVASKELQQPGSARSTRHLEI--ELPKEASYQEGDHLGVIPRNYEGIVNRV 714
                                                                                                                                               TARF--GLDASQQIRLEAEEEKLAHLPLAKTV---SVEELLQY-VELQDPVTRTQLRAMA 768
                                                                                                                                                                                                                                                                                    769 AKTVCPPHKVELEALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRY 828
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                                                                              568 AFRSWAVQTFKAACETFDVRGKQHIQIPKLYTSNVTWDPHHYRLVQDSQPLDLSKALSSM 727
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                                        TYEEWREHMWS-----DVAAYFNLDIENSEDNKSTLS---LQFVDSAADMPLAK----M
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11.9%; Score 650; DB 10;
Best Local Similarity 30.3%; Pred. No. 5.9e-39;
Matches 195; Conservative 112; Mismatches 272;
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; ORGANISM: Induced Human Hepatocyte RNA
US-09-992-056-2
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: Nussler, Andreas K.
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EE-LENAQSEGIITLHTAFSRMPNQPKTYVQHVMEQD--GKKLIELLDQGAHFYICGDGS 1003
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                                     Length 1203;
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COTHER INFORMATION: Human nitric oxide synthase US-10-224-249-15
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Publication No. US20030087867A1
GENERAL INFORMATION:
APPLICANT: Vogels, Ronald V.
APPLICANT: Verlinden, Stefan F.F.
TITLE OF INVENTION: Gene therapy for enhancing TITLE OF INVENTION: Gene therapy for enhancing TITLE OF INVENTION: Gene therapy for enhancing TITLE REFERENCE: 2183-5233US
CURRENT APPLICATION NUMBER: US/10/224,249
CURRENT FILING DATE: 2000-07-07
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 16
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G-IITLHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLM 1014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  540 PPDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAF---IDETLAAKGAEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 FAEYAE---GDDGTGTLDEDFMAWKDNVFDALKNDLNFEEKELKYEPNVKLTERDDLSAA
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                                                                                                                                                                                                                                                                                                                                   Length 679
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                                                                                                                                                                                                                                                                                                                                   Score 598; DB 9;
Pred. No. 1.8e-35;
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CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VEFSION 3.1
SEQ ID NO 117
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US-10-139-031-117
Sequence 117, Application US/10139031
Publication No. US20030049822A1
GENERAL INFORMATION:
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27.2%;
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US-10-138-838-117
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APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
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                                                                                                                                                                                        LENGTH: 679
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APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Coper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
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                                             Gaps
         ed. No. 7e-36;
Mismatches 254; Indels 155;
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CURRENT APPLICATION NUMBER: US/10/138,838
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               Pred.
                                       191; Conservative 115;
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APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
            26.7%;
            Best Local Similarity
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                                       Matches
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APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF THE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
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       648 KIVAKSREISEDKAAELVKSWKVQNRYQEDVW 679
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CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
                                                                                                                                                                                        Sequence 117, Application US/10138905
Publication No. US:20030068800A1
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Brenner, Alfred A.
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APPLICANT: Craft, David L.
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Eshoo, Mark
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LENGTH: 679
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TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: TO TOCHROME P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX (TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,031
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR ELILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
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Best Local Similarity 27.2%; Pred: No. 1.8e-35;
Matches 188; Conservative 130; Mismatches 282
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       Krishna M.
Madduri, Krishna M
Cornett, Cathy A.
Brenner, Alfred A.
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SOFTWARE: PatentIn version 3.1
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                                                                                                             Tang, Maria
Loper, John C.
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APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Glesson, Marin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOR
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX O
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
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   PLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEE-LENAQSE 955
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Matches 188; Conservative 130; Mismatches 282;
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APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
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APPLICANT: Loper, John C.
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROWE P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDG
TITLE OF INVENTION: CRICKING THE OMEGA HYDROXYLASE COMPLEX OF CHILLE OF INVENTION: TROPICALIS AND PROTEINS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/138,916
CURRENT FILING DATE: 2002-05-03
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 1999-04-30
                                                                                                               G-IITLHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLM 1014
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 RPVTGVVTNLLKNVEIVQNKTGEKPLVHYDLSGPRGKFNKFKLPVHVRRSNFKLPKNSTT 527
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                                   PLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEE-LENAQSE
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5 KIDLYVIITLVVAVAAYFAKNQFLDQPQDTGFLNTDSGSNSRDVLSTLKKNNKNT--LLL
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Publication No. US20030073220A1
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APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Madduri, Krishna M.
APPLICANT: Denoer, Alfred A.
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SOFWARE: Patentin version 3.1
SEQ ID NO 117
LENGTH: 679
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APPLICANT:
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TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX O
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
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CURRENT APPLICATION NUMBER: US/10/139,031
CURRENT FILING DATE: 2002-05-03
FILE REFIRENCE TO NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
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APPLICANT: Craft, David L.
APPLICANT: Exich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
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Loper, John C.
Gleeson, Martin
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APPLICANT: Craft, David L.

APPLICANT: Craft, David L.

APPLICANT: Eshoo, Mark

APPLICANT: Eshoo, Mark

APPLICANT: Eshoo, Mark

APPLICANT: Cathy A.

APPLICANT: Cronett, Cathy A.

APPLICANT: Tang, Maria

APPLICANT: Tang, Maria

APPLICANT: Tang, Maria

APPLICANT: Tang, Maria

APPLICANT: Gleeson, Martin

ITILE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME

ITILE OF INVENTION: P450 OXIDOREDUCTASE

ITILE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF CURRENT FILING DATE: 2002-05-03

FILE REFERENCE: 1010-16

CURRENT APPLICATION NUMBER: US/10/138,838

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US/09/976,800

PRIOR FILING DATE: 2001-10-12

NUMBER OF SEO ID NOS: 118

SOFTWARRE: Patentin version 3.1
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   IADRGEADASDDFEGTYEE ----WREHMWSDVAAYFNLD-----
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Publication No. US20030049821A1
GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: CANDIDATROPICALIS
US-10-138-838-83
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Matches 188; Conserv
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US-10-138-905-83
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                                                                                                                                                                                                                                                   SOVSLGEPNKKYINSEGIDLTKG-PFDHTH-PYLARITETRELFS-SKDRHCIHVEFDI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PK-EASYQEGDHLGVIPRNYEGIVNRVTARFGLDASQQIRLEAEE-EKLAHLPLAKTVSV 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SESNLKYTTGDHLAIWPSNSDENIKQFAKCFGLEDKLDTVIELKALDSTYTIPFPTPITY 351
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5 KLDLYVIITLVVAVAAYFAKNQFLDQPQDTGFLNTDSGSNSRDVLLTLKKNNKNT--LLL
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                                                                                                                                                                        430 ELDIKETLTLKPEGFVVKAKSKKI----PLGGIPSPSTEQSAKKVRKKAENAHNTPLLVL
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                                                                                                                                                Gaps
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                                                                                                                   Length 679;
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                                                                                                                Query Match 10.9%; Score 597; DB 9; L
Best Local Similarity 27.2%; Pred. No. 2.1e-35;
Matches 188; Conservative 130; Mismatches 282;
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Publication No. US20030068800A1
GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Eirich, Dudley
APPLICANT: Eirich, Dudley
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
             PatentIn version 3.1
                                                                    ; ORGANISM: CANDIDATROPICALIS
US-10-139-031-83
NUMBER OF SEQ ID NOS: 118
                                          619
             SOFTWARE: Page SEQ ID NO 83
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APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Glesson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: TROPICALIS AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERBNCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/138,905
CURRENT FILING DATE: 2002-05-03
PRIOR PILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentr
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Search completed: May 29, 2003, 08:27:08 Job time: 35 secs

us-10-031-146-2\_1.rapb

Title: Perfect score: Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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APPLICANT: PLEISS, Juergen
APPLICANT: SCHWANEBERG, Ulrich
APPLICANT: SCHWATT, Jutta
APPLICANT: SCHWATT. Jutta
TITLE OF INVENTION: Organic substrates
FILE REFERENCE: 50915
CURRENT APPLICATION NUMBER: US/10/031,146
CURRENT APPLICATION NUMBER: PCT/FP 00/07253
PRIOR APPLICATION NUMBER: PCT/FP 00/07253
PRIOR FILING DATE: 2000-07-27
NUMBER: Word Perfect version 6.1
SEQ ID NO 2.
                                                                                           Sequence 4, April Sequence 6, Appli Sequence 139768, Sequence 139768, Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 6, Appli Sequence 13976, A Sequence 3, Appli Sequence 16499, Sequence 16499, Sequence 9, Appli Sequence 10, Appli Sequence 29265, A Sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 54, Appl
Sequence 12987, A
Sequence 56962, A
Sequence 118779,
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                                                                    Sequence 21,
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5 US-10-125-640-2

6 US-10-201-213-2

4 US-10-018-730A-4

4 US-10-018-730A-4

6 US-10-018-730A-4

6 US-10-018-730A-4

1 US-09-96-11954-6

PCT-USO2-11954-7

1 US-09-791-537-139768

1 US-09-791-537-139586

1 US-09-791-537-13071

1 US-09-791-537-14649

1 US-09-791-537-14649

1 US-09-791-537-14649

1 US-09-791-537-130911

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1 US-09-791-537-16501

1 US-09-791-537-16501

2 US-08-882-163-9

2 US-08-882-163-9

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3 US-09-791-537-10501

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4 US-10-021-425-55

4 US-10-021-425-55

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6 US-09-791-537-10974

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Sequence 35, Appl
Sequence 2, Appli
Sequence 53927, A
Sequence 9, Appli
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4145.278 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                          1 TIKEMPQPKTFGELKNLPLL......RLWLQQLEEKGRYAKDVWAG 1048
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1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*

8: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*

9: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*

10: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

11: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

12: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

13: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*

14: /cgn2_6/ptodata/1/paa/US088_COMB.pep:*

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                                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-031-241-35
US-10-031-695-2
PCT-USO2-11954-2
US-09-791-537-53927
US-09-791-1546-9
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Listing first 45 summaries
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Sequence 35, Application US/10031241 GENERAL INFORMATION:
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                   DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRA
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US-10-031-241-35

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biochemic ö 120 120 180 180 240 240 300 540 540 900 420 420 480 480 900 999 099 720 720 780 9 9 theKDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD 1 TIKEMPOPKTFGELKNLPLLNTDKPYQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRA LDEAMNKLORANPODPAYDENKROFOEDIKVMNDLVDKIIADRKASGEOSDDLLTHMLNG FDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKAENAHVT PLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP PDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADR DASQQIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVEL 1 TIKEMPOPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE ACDESRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMV HRDKT IWGDDVEEFRPERFENPSAIPQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKH FDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNT GEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG AFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL Gaps 무 nse Length 1048 ö and its Indels enzymes 24; ö APPLICANT: Schmid, Rolf D.
TITLE OF INVENTION: Electron donor system for en:
TITLE OF INVENTION: conversion of substrates
FILE REFERENCE: M/40076
CURRENT APPLICATION NUMBER: US/10/031,241
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: PCT/FP00/07251
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 35 В Query Match 100.0%; Score 5457; Best Local Similarity 100.0%; Pred. No. 0; Matches 1048; Conservative 0; Mismatches 661 721 g à

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0y 781 EALLEKQAYKEQVLAKRLTMLIDD DB 721 DASQQIRLEABEBEKLAHLIDLELD DB 781 EALLEKQAYKEQVLAKRLTMLIDD 781 EALLEKQAYKEQVLAKRLTMLIDD 781 EALLEKQAYKEQVLAKRLTMLIDD 841 QASITVSVVSGEAWSGYGEYKGUK 1

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P14779
NUMBER: GenBank
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; DATABASE ACCESSION NUMBER: GenBa
; DATABASE ENTRY DATE: 1990-04-01
; RELEVANT RESIDUES: (1)..(1049)
PCT-US02-11954-2
                               Ouery Match 100.0%;
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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMMENSIONAL STRUCTUR
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 55927
LENGTH: 1049
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s; Pred. No. 0;
0; Mismatches
                                                          HQVSEADARLWLQQLEEKGRYAKDVWAG 1048
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llarity 100.0%;
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US-09-791-537-53927
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APPLICANT. ...
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	Qy         301 PVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTYLGGEYPLEKGDELAVLIPQL 360	Qy 421 FDFEDHTNYELDIKETLTIKPEGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNT 480 	QY 481 PLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP 540	QY 541 PDNAKQEVDWLDQASADEVKGVRYSVFGCGGKNWATTYQKVPAFIDETLAAKGAENIADR 600 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	QY 601 GEADASDDFEGTYEEWREHAWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG 660	Qy 661 AFSTNVVASKELQOPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL 720	QY 721 DASQQIRLEAEBERLAHLPLAKTVSVEELLQYVELQDPVIRTQLRAMAAKTVCPPHKVEL 780	QY 781 EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEK 840	QY 841 QASITVSVVSGEAMSGYGEYKGIASNYLAELQEGDTITCFISTPOSEFTLEKDPETPLIM 900	QY . 901 VGPGTGYAPFRGFVQARKQLKEQGOSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL 960	QY 961 HTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQWAPAVEATLMKSYADV 1020	Qy 1021 HQVSEADARIMILQQLEEKGRYAKDVWAG 1048 	RESULT 7 US-10-125-640-2 ; Sequence 2, Application US/10125640 ; GREERAL INFORMATION: ; APPLICANT: Cirino, Patrick C. ; APPLICANT: Arnold, Frances H. ; TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS	; FILE REFERENCE: 4058/JK237-US3 ; CURRENT APPLICATION NUMBER: US/10/125,640 ; CURRENT FILING DATE: 2002-04-16 ; PRIOR APPLICATION NUMBER: 60/284,215 ; PRIOR FILING DATE: 2001-04-16 ; PRIOR APPLICATION NUMBER: 60/288,636
QY         601 GEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG 660           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	721 DASQOIRLEAEEEKLAHLPLAKTVSVEELLÖYVELQDPVTRTOLRAMAAKTVCPPHKVEL 722 DASQOIRLEAEEEKLAHLPLAKTVSVEELLÖYVELQDPVTRTOLRAMAAKTVCPPHKVEL 722 DASQOIRLEAEEEKLAHLPLAKTVSVEELLÖYVELQDPVTRTOLRAMAAKTVCPPHKVEL 781 EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEK	OY 841 QASITVSVVSGEAWSCYGEVKGIASNYLAELQEGDTITCFISTPQSEFLEPKDPETPLIM 900  B42 QASITVSVVSGEAWSCYGEVKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 900  B42 QASITVSVVSGEAWSCYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM 901		MKSYADV 			JOUGHT 146.9 Application US/10031146 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: HAUBR, Berhard	** APPLICANT: PLEISS, JUEGEN ** APPLICANT: SCHWANEBERG, JULICH ** TITLE OF INVENTION: NOVEL cytchrome P450 monooxygenases and their use for the oxidat	FILE REFERENCE: 5091: CURRENT APPLICATION I CURRENT FILING DATE:	U	; LENGTH: 1049 ; TYPE: PRT ; ORGANISM: Bacillus megaterium	Query Match 100.0%; Score 5457; DB 24; Length 1049; Best Local Similarity 100.0%; Pred. No. 0; Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY         1 TIKEMPQPRIFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE 60	OY 121 DIAVOLVOKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDOPHPFITSMVRA 180

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                                                                                ORGANISM: Bacillus megaterium
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank / P14779
DATABASE ENTRY DATE: 1990-04-01
RELEVANT RESIDUES: (1)..(1049)
                                                                                                                                                        100.0%; Score 5457; 100.0%; Pred. No. 0;
                                                                                                                                                                             0; Mismatches
        PRIOR APPLICATION NUMBER: 60/340,602 PRIOR FILING DATE: 2001-12-12 NUMBER OF SEQ ID NOS: 12 SOFTWARE: PATENTIN VERSION 3.1 SEQ ID NO 2
PRIOR FILING DATE: 2001-05-03
                                                                                                                                                                  Best Local Similarity 100.
Matches 1048; Conservative
                                                             LENGTH: 1049
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                                                                        TYPE: PRT
                                                                                                                                                          Query Match
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APPLICANT: Farinas, Edgardo
APPLICANT: Glieder, Anton
APPLICANT: Glieder, Anton
APPLICANT: Glieder, Anton
APPLICANT: Arnold, Frances
APPLICANT: Arnold, Frances
APPLICANT: Schwanberg, Ulrich
TITLE OF INVENTION: IMPROVED CYTOCHROME P450 OXYGENASES
FILE REFERENCE: 3369/IK238-US2,
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 60/306,766
PRIOR FILING DATE: 2001-07-20
PRIOR FILING DATE: 2001-07-20
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
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100.0%; Pred. No. 0;
:ive 0; Mismatches
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DATABASE ACCESSION NUMBER: Genbank / P14779
DATABASE ENTRY DATE: 1990-04-01
RELEVANT RESIDUES: (1)..(1049)
                                                                                                                                                                                                                                                                                                              HOVSEADARLWLQQLEEKGRYAKDVWAG 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10201213 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 1048; Conservative
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ö 180 240 300 360 420 480 840 120 121 181 241 301 361 421 481 540 541 9 601 9 661 720 721 780 781 841 900 901 960 961 9 61 HRDKTIWGDDVEEFRPERFENPSAIPQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKH ACDESRFDKNLSOALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMV DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRA L.DEAMNKLORANPDDPAYDENKROFOEDIKVMNDLVDKIIADRKASGEOSDDLLTHMLNG KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD PVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDELMVLIPQL PAPSYKQVKQLKYVGMVLNEALRLMPTAPAFSLYAKEDTVLGGEYPLEKGDELMVLIPQL FDFEDHTNYELDIKETLILKFEGFVVKAKSKKIPLGGIPSPSTEQSAKKARKKAENAHNT PLLVLYGSNWGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHP PDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADR GEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG DASQQIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVEL DASQOIRLEAEEEKLAHLPLAKTVSVEELLOYVELQDPVTRTQLRAMAAKTVCPPHKVEL QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM VGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL AFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL EALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEK TIKEMPOPKIFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKE FDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNT Gaps ; 0 1049;

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HTAFSRMPNOPKTYVOHVMEODGKKLIELLDOGAHFYICGDGSOMAPAVEATLMKSYADV 1020
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GENERAL INFORMATION:
APPLICANT: CLIINO, PATITICA C.
APPLICANT: ALALOIG FRANCES H.
ITILE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS
FILE REFERENCE: 4058/28237-W00
CURRENT APPLICATION NUMBER: PCT/US02/11954
CURRENT APPLICATION NUMBER: 60/284,215
PRIOR APPLICATION NUMBER: 60/284,215
PRIOR PELING DATE: 2001-04-16
PRIOR FILING DATE: 2001-05-03
PRIOR FILING DATE: 2001-05-03
PRIOR PLICATION NUMBER: 60/380,636
PRIOR PLICATION NUMBER: 60/340,602
PRIOR PELING DATE: 2001-12-12
NUMBER OF SEC ID NOS: 12
SOFTWARE: PATENTIN VERSION 3.1
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DATABASE ENTRY DATE: 2001-10-16
RELEVANT RESIDUES: (1)..(1061)
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PUBLICATION INFORMATION:
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                                                                                                                                                                        Sequence 4, Application US/10018730A
GENERAL INFORMATION:
APPLICANT: Luet, Wong
TITLE OF INVENTION: PROCESS FOR OXIDISING AROMATIC COMPOUNDS
FILE REFERENCE: P0235303, / 10112404 / N.76277B
CURRENT APPLICATION NUMBER: US/10/018,730A
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 12999-06-18
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: PCT/GB00/02379
PRIOR FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 18
COFFWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1049;
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Pred. No. 0;
0; Mismatches
                                                                      1021 HQVSEADARLWLQQLEEKGRYAKDVWAG 1048
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Best Local Similarity 99.8%;
Matches 1046; Conservative
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US-10-018-730A-4
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                PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS
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                                                                                                                                                                                                                                                                                                                                    ch 60.7%; Score 3314; DB 1; 11 Similarity 59.5%; Pred. No. 1e-287; 628; Conservative 156; Mismatches 259;
            TITLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROM CURRENT APPLICATION NUMBER: PCT/USOZ/11954 CURRENT FILING DATE: 2002-04-16 PRIOR EXPLICATION NUMBER: 60/284,215 PRIOR EXPLICATION NUMBER: 60/284,215 PRIOR FILING DATE: 2001-04-16 PRIOR APPLICATION NUMBER: 60/288,636 PRIOR APLICATION NUMBER: 60/288,636 PRIOR APLICATION NUMBER: 60/288,636 PRIOR APLICATION NUMBER: 60/340,602 PRIOR FILING DATE: 2001-02-12
                                                                                                                                                                                                                                ORGANISM: Bacillus subtilis
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank / D69799
DATABASE BWTRY DATE: 2000-07-28
RELEVANT RESIDUES: (1)..(1061)
                                                                                                                                                           NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
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Matches 628;
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                                          QLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRALDEA
                                                                                                   MNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSD-DLLTHMLNGKDP
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PCT-US02-11954-7; Sequence 7, Application PC/TUS0211954; GENERAL INFORMATION: ; APPLICANT: Cirino, Patrick C.
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715 TARFGLDASQQIRLEAEBEKLAHLPLAKTVSVEELLQY-VELQDPVTRTQLRAMAAKTVC 773      :	ζζ Op	364 KTIWGDDVEEFRPERFENPSAIPQHAFKPFGNGQRACIGQQFALHEATLVLGAMLKHFDF 423 :
774 PPHKVELEALLEKQAYKEOVLAKRITMLELLEKYPACEMKFSEFIALLPSIRPRYYSISS 833 	Qy	424 EDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGIPSPSTEGSAKKVRKKAENA 477
834 SPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKD 893 	Qy	478HNTPLLVLYGSNMGTABGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTAS 535 :
894 PETPLIMVGPGTGVAPFRGFVQARKOLKEOGOSLGEAHLYFGCRSPHEDYLYQEELENAQ 953      :	Qy	536 YNGHPPDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAE 595 
954 SEGITILHTANSRMPNOPKTYVOHVMEQDGKKLIELLDQGAHFYICGDGSOMAPAVEATL 1013 1 : :	Qy	596 NIADRGEADASDDFEGTYEEWREHMWSDVAAYFNLDI-ENSEDNKSTLSLQFVDSAADMP 654 :
1014 MKSVADVHQVSEADARLWIQQLEEKGRYAKDVWAG 1048 	Qy	655 LAKMHGAFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRV 714   :: :: :: :          :
537-139768	Qy Db	715 TARFGLDASQQIRLEAEBERLAHLPLAKTVSVEELLQY-VELQDPVTRTQLRAMAAKTVC 773
Sequence 13/06, Application US/U9/9153/ GENERAL INFORMATION: APPLICANT: Bionomix, inc. APPLICANT: Debe, Derek	. Qy	774 PPHKVELEALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYSISS 833
AFFILCANI: DANIZE, JOSEPH TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE TITLE OF INVENTION: METHODS OF USE THEREOF FILE REFERENCE: 261/210	QY	834 SPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKD 893      ::
CORRENT FILING DATE: US/US/191/31/ NUMBER OF SEQ ID NOS: 153055 SOFTWARE: Petentin version 3.0	QY	894 PETPLIMVGPGTGVAPFRGFVQARKQLKEGGGSLGEAHLXFGCRSPHEDYLXQEELENAQ 953 
; LENGTH: 1061 ; TYPE: PRT ; ORGANISM: Bacillus subtilis US-09-537-139768	Qy	954 SEGIITLHTAFSRAPNQEKTYQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATL 1013 :  :
Query Match  Query Match  Best Local Similarity 59.5%; Pred. No. 1e-287;  Matches 628; Conservative 156; Mismatches 259; Indels 12; Gaps 6;	QQ .	1014 MKSYADVHQVSEADARLWLQQLEEKGRYAKDVWAG 1048  :        : :   :             1026 QKAYQAVHGTGEQEAQNWLRHLQDTGMYAKDVWAG 1060
5 MPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKEACDE 64 	RESUI US-10	RESULT 14 US-10-125-640-6 ; Sequence 6, Application US/10125640
65 SRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMVDIAV 124     ::  :  :   :	GEN	ERRAL INFORMATION: PLICANT: CITIO, PALTICK C. PLICANT: Arnold, Frances H. TLE OF INVENTION: PEROXIDE-DRIVEN CYTOCHROME P450 OXYGENASE VARIANTS
125 QLVQKWERLNADEHIEVPEDMTRLTLDTIGLGGFNYRENSFYRDQPHPFITSMVRALDEA 184   -		FILE REFERENCE: 4058/1K237-US3 CURRENT APPLICATION NUMBER: US/10/125,640 CURRENT FILING DATE: 2002-04-16 PRIOR APPLICATION NUMBER: 60/284,215
185 MNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSD-DLLTHMLNGKDP 243 		LIOR FILING DATE: 2001-04-16 LIOR APPLICATION NUMBER: 60/288,636 LIOR FILING DATE: 2001-05-03 LIOR APPLICATION NUMBER: 60/340,602
244 ETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLYKNPHVLQKAAEEAARVLVDPVP 303 	PR ; NU ; SC ; SEQ	PRIOR FILING DATE: 2001-12-12 NUMBER OF SEQ ID NOS: 12 SOFTWARE: Patentin version 3.1 SEQ ID NO 6
304 SYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDELMVLIPQLHRD 363 :     :   :  :		LENGTH: 1061 TYPE: PRT ORGANISM: Bacillus subtilis

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Query Match 60.7%; Sc
Best Local Similarity 59.5%; Pr
Matches 628; Conservative 156;
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SOFTWARE: PatentIn version 3.1
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                                                                                        QLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRALDEA
                                                                                                                                                       MNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSD-DLLTHMLNGKDP
                                                                                                                                                                                        KTIWGDDVEEFRPERFENPSAIPQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKHFDF
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                                                                Gaps
                                                                12;
                                                 Length 1061;
                                                                Indels
                                              tch 60.7%; Score 3314; DB 25; al Similarity 59.5%; Pred. No. 1e-287; 628; Conservative 156; Mismatches 259;
      DATABASE ACCESSION NUMBER: GenBank / 008394
DATABASE ENTRY DATE: 2001-10-16
RELEYANT RESIDUES: (1)..(1061)
PUBLICATION INFORMATION
                        ; RELEVANT RE:
US-10-125-640-6
                                               Query Match
Best Local S:
Matches 628
                                                                                                                65
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SEGIITLHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATL 1013
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; GENERAL INFORMATION:
APPLICANT: CILINO, PATICK C.
APPLICANT: AINOIG, FRANCES H.
TITLE OF INVENTION: PEROXIDE-DRIVEN CYTCCHROME P450 OXYGENASE VARIANTS
FILE REFERENCE: 4058/1K237-US3
CURRENT APPLICATION NUMBER: US/10/125,640
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 60/284,215
PRIOR APPLICATION NUMBER: 60/289,636
PRIOR PILING DATE: 2001-04-16
PRIOR PELING DATE: 2001-03-03
PRIOR PELICATION NUMBER: 60/340,602
PRIOR PELICATION NUMBER: 60/340,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMVDIAV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRALDEA 184
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Pred. No. 1e-287;
5; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBLICATION INFORMATION:
DATABASE ACCESSION'NUMBER: Genbank / D69799
DATABASE ENTRY DATE: 2000-07-28
RELEVANT RESIDUES: (1)..(1061)
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YNGHPPDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAE 595
                                        715 TARFGLDASQQIRLEAEEEKLAHLPLAKTVSVEELLQY-VELQDPVTRTQLRAMAAKTVC 773
                                                                                                                                                             PPHKVELEALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYSISS 833
                                                                                                                                                                                            SPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKD 893
                                                             --HNTPLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTAS
                                                                                              LAKMHGAFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRV
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Search completed: May 29, 2003, 08:25:33 Job time : 169 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 29, 2003, 08:22:16; Search time 54 Seconds
(without alignments)
4017.377 Million cell updates/sec
Title: US-10-031-146-2
Perfect score: 5457
Sequence: 1 TIKEMPOPKTFGELKNLPLL......RLWLQQLEEKGRYAKDVWAG 1048
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 995812 seqs, 207002235 residues
Total number of hits satisfying chosen parameters: 995812
```

Pending\_Patents\_AA\_New:\*

1: /cgn2\_6/ptodata/2/paa/VCT\_NEW\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep:\*

3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep:\*

4: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:\*

6: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:\*

7: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:\*

7: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:\*

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 24, Appl Sequence 8117, Ap Sequence 11638, A Sequence 1155, A Sequence 23, Appl Sequence 12757, A Sequence 572, App Sequence 572, Appl Sequence 712, Appl Sequence 19724, Sequence 70174, A 8116, Ap 8116, Ap 1, Appli 4, Appl 4, Appl 77338, 86297, A 86297, A 2398Z, A Appli 14960, A Appl Description Sequence Sequence S Sequence US-10-219-051B-12757 US-60-440-068-572 US-10-424-599-187294 US-10-425-114-70174 US-10-424-599-191313 US-10-188-523B-14 US-10-188-523C-14 US-10-424-599-177338 US-10-156-761-14954 US-10-219-051B-11638 US-10-219-051B-12755 US-09-724-676A-86297 US-60-452-680-23982 US-60-453-135-14960 US-60-453-050-14960 -09-661-258-1 -09-751-708A-124 SUMMARIES Match Length DB . Query Score 2420.5 1945.5 953.5 777.5 777.5 769 767 675 675 675 665.5 665.5 661 661 728.5 712.5 712.5 710 705.5 705.5 688 688 Result

Sequence 5970, Ap Sequence 313, App Sequence 4154, Ap	041	Sequence 3, Appli Sequence 18506, A Sequence 11109, A	Sequence 11109, A Sequence 5820, Ap Sequence 5820, Ap	Sequence 117, App Sequence 3, Appli Sequence 83, Appl	Sequence 2, Appli Sequence 11, Appl Sequence 118, App Sequence 86275, A
US-09-949-016-5970 US-10-126-052A-313 US-10-369-493-4154	6 US-10-282-122A-61918 · 6 US-10-369-493-4874 6 US-10-369-493-7634	US-09-661-258-3 US-60-452-680-18506 US-60-453-135-11109	US-60-453-050-11109 US-60-455-444-5820 US-60-465-241-5820	US-10-405-660-117 US-10-272-017A-3 US-10-405-660-83	US-10-272-017A-2 US-10-400-902-11 US-10-405-660-118 US-09-724-676-86275
	1042 592 592 6				
12.0 12.0 11.6	11.3	11.2	11.2 11.2 11.2	11.0 10.9 10.9	10.9 10.9 10.9
656 656 632.5	614.5 609.5 609.5	608.5 608.5 608.5	608.5 608.5 608.5	598 597 597	. 596 594 594 594
27 28 29	331 321	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	36 38	39 40 41	444 444 544

## ALIGNMENTS

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                                    Sequence 24, Application US/10214446

GENERAL INFORMATION:
APPLICANT: Wether, David
APPLICANT: Hitchman, Tim
APPLICANT: Pujol, Catherine
APPLICANT: Pujol, Catherine
APPLICANT: Richardson, Toby
APPLICANT: Richardson, Toby
APPLICANT: Richardson, Toby
TITLE OF INVENTION: P450 ENZYMES, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: P450 ENZYMES, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: P450 ENZYMES, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: THEM AND METHODS OF MAKING AND USING THEM
FILE REFERENCE: 09010-500001
CURRENT APPLICATION NUMBER: US/10/214,446
CURRENT FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 59
SOFTWARRE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 44.4%; Score 2420.5; DB 6; Length 1077; Best Local Similarity 47.0%; Pred. No. 6.5e-202; Matches 506; Conservative 170; Mismatches 365; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Obtained from an environmental sample US-10-214-446-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Unknown
US-10-214-446-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182
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APPLICANT: INEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: HORIKAMA, JUN
APPLICANT: HORIKAMA, HIROSHI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: HATTORI, MASAHIRA
ITLE OF INVERTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30 PRIOR FILING DATE: 2001-05-30 PRIOR APPLICATION NUMBER: JP 2001-272697

17; 222 340 111 171 PFLNALLQALVESLRRSQELPVMTKMRKA--DDKKYREN-----IRLMRDLVENVIKE 230 281 290 350 393 404 453 513 524 572 584 632 643 682 702 742 762 796 822 856 882 YGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGFVQA 916 25 9 7 QPKT-------FGELKNLPLLNTDKPVQALMKIADELGE-IFKFEAPGRVTRYL HLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGLDASQQIRLEAEEEKLAHLPLAK SSQRLIKEACDESRFDKNLSQA-LKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQA MKGYHAMMVDIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPH PFITSMVRALDEA------MNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIAD RK-ASGEQSDDLLTHMLNGKDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLV KNPHVLQKAAEEAARVLV-DPVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTV 351 IGGCYGLKKGARVNILEGPLHTHPKAWE-----RPEEFDINRWLPENRVNHHPHAYKPF PLGGIPSPSTEQSAKKVRKKAENAHNTPLLVLYGSNMGTAEGTARDLADIAMSKGFAPQV : |: |: || || || || || HERTYFGAADLQTDDTQAQAAVSGVGVNLTVAYGSSLGSCEDLARTIADRGERSGFGTTL 514 ATLDSHAGNLPREGAVLIVTASYNGHPPDNARQFVDWLDQASAD-EVKGVRYSVFGCGDK 763 PVTTGLLFTEFVELQDVATRSQIQELAEHTQCPWTRPQLQAYTADTAEAEERYQKEILGK RVSVLNLLERFPAVELPLAVFLEMMGPIRPRFYSISSSPLANPRHVRLTVGLLEGPALSG --HAFKPF GNGQRACIGQQFALHEATLVLGMMLKHFDFEDHTNYELDIKETLTLKPEGFVVKAXSKKI 573 NWATTYQKVPAFIDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFNLDI EKQAYKEQVLAK RLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEKQASITVSVVSGEAWSG Length 1073; ENSEDNKSTLSLQFVDSAADMPLAKMHGAFSTNVVASKELQQPGSA----LGGEYPLEKGDELMYLIPQLHRDKTIWGDDVEEFRPERFENPSAIPQ----TVSVEELL-QYVELQDPVTRTQLRAMAAKTVCPPHKVELEALL--; 408; 35.7%; Score 1945.5; DB 6 llarity 38.2%; Pred. No. 2.4e-160; Conservative 195; Mismatches 408; ; TYPE: PRT ; ORGANISM: Streptomyces avermitilis US-10-156-761-8117 2001-08-02 NUMBER OF SEQ ID NOS: 15109 SEQ ID NO 8117 Query Match Best Local Similarity Matches 417; Conserv PRIOR FILING DATE: 857 53 121 172 180 223 231 282 291 341 394 405 454 465 585 633 644 683 703 743 823 197 LENGTH: õ a ö d a ŏ g g õ 셤 ŏ g ð a ð 셤 ŏ 셤 ò a à g ò g ò a 셤 ð ò ò ò

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RKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITLHTAFSRMPNQPKTYVQ
                                                            2 IKEMPOPKTFGELKNLPL-----LNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQ
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43.1%; Pred. No. 3.6e-74;
tive 79; Mismatches 174;
                                                                                                                                                                                                                                                                                                      APPLICANT: IKEDA, HARUO

APPLICANT: ISHIRAWA, JUN

APPLICANT: HORIRAWA, HINOSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: HATTORI, WASAHRA

TITLE OF INVENTION: NOVEL POLYNCLEOTIDES

FILE REFERRNCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30

PRIOR FILING DATE: 2001-05-30

SEQ ID NO 14954

LENGHH: 504
                                                                                                                                                                                                                                                               Sequence 14954, Application US/10156761
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
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US-10-156-761-14954
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1063 ADERYQODVFA 1073
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                  467
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410 ATLVLGMMLKHFDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGIPSPSTEQSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 677;
                                                                                                                                                                               AFPLICAMY: INCEPTION: Nucleotide sequences involved in pain TITLE OF INVENTION: Nucleotide sequences involved in pain FILE REFERENCE: LeA 3563 Foreign Countries CURRENT APPLICATION NUMBER: US/10/219,051B CURRENT FILING DATE: 2003-05-09 PRIOR APPLICATION NUMBER: US 60/312,147 PRIOR PLING DATE: 2001-08-14 PRIOR FILING DATE: 2001-11-01 PRIOR PLING DATE: 2001-11-26 NUMBER OF SEQ ID NOS: 14715 SCPURARE: Perl script SCPURARE: Perl script SCPURARE: Perl script SCPURARE: Perl SCRIPT
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ches 263;
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                                                                                                                                                    APPLICANT: The General Hospital Corporation doing APPLICANT: Hospital / Bayer AG
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; DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-11638
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14.2%; Score 777.5; I
Best Local Similarity 32.2%; Pred. No. 1.6e
Matches 211; Conservative 111; Mismatches
                                                                                                                    Sequence 11638, Application US/10219051B GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                       APPLICANT: Novartis AG
TITLE OF INVENTION: Compositions and Methods for Halegenation Reactions
FILE REFERENCE: S-31082A
CURRENT PELINGN NUMBER: US/10/148,907A
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 60/228801
PRIOR APPLICATION NUMBER: US 60/219343
PRIOR FILING DATE: 1999-112-15
PRIOR FILING DATE: 1000-01-03
PRIOR FILING DATE: 2000-01-03
                                                                                                                                                      993 -GAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047
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                                                                                                                                                                                                                                                                                                     Sequence 23, Application US/10148907A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                  US-10-148-907A-23
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LENGTH: 682
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GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation doing business as Massachusetts General
APPLICANT: The General Hospital Corporation doing business as Massachusetts General
APPLICANT: Hospital / Bayer AG
FILE REFERENCE: LeA 35693 Foreign Countries
CURRENT APPLICATION NUMBER: US/10/219,051B
CURRENT FILING DATE: 2003-05-09
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-11-01
PRIOR FILING DATE: 2001-11-01
PRIOR FILING DATE: 2001-11-10
PRIOR FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 14715
SEQ ID NO 12755
LENGTH: 677
FGCRSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDO 992
                                       YGCRRSDEDYLYREELARFHKDGALTQLNVAFSR-EQAHKVYVQHLLKRDREHLWKLIHE 621
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                                                                                   -GAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047
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DATABASE ACCESSION NUMBER: SWISS-Prot / AAA41064
DATABASE ENTRY DATE: 2002-06-15
US-10-215-051B-12755
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TITLE OF INVENTION: POLYMUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE TITLE OF INVENTION: POLYPEPTIDES ASSOCIATED WITH THE TITLE OF INVENTION: NE-KB PATHWAY FILE REFERENCE: 3053-4191
CURRENT APPLICANTION NUMBER: US/60/440,068
CURRENT FILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 746
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                                                      ITCFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGC
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                                                                                                                                                                                                                    14.1%; Score 767; DB 7; Length 677; 32.4%; Pred. No. 1.3e-57; Live 113; Mismatches 264; Indels
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Sequence 572. Application US/60440068
SENERAL INFORMATION:
APPLICANT: NADLER, STEVEN G.
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US-60-440-068-572
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Matches 211;
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LENGTH: 677
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                                                                                                                                                                                                                                                                                                APPLICANT: The General Hospital Corporation doing business as Massachusetts General APPLICANT: The General Hospital / Bayer AG
TITLE OF INVENTION: Nucleotide sequences involved in pain
FILE REFERENCE: LeA 35693 Foreign Countries
CURRENT APPLICATION NUMBER: US/10/219,051B
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: US 60/312,147
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-11-01
PRIOR FILING DATE: 2001-11-26
NUMBER: OF SEQ ID NOS: 14715
SOFTWARE: Perl script
SEQ ID NO 12757
                                                                     980 EQDGKKLIELLDQ-GAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEK 1038
 KEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVM 979
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                                   ROOGKEVGETLLYYGCRRAAEDYLYREELAGFOKDGTLSQLNVAFSREQAQ-KVYVQHLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                444 FVVKAKSKKIP----LGGIPSPSTEQS-AKKVRKKAENAHNTPLLVLYGSNMGTAEGTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 FLFRKKKEEVPEFTKIQTLTSSVRESSFVEKMKKTGRN----IIVFYGSQTGTAEEFAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 DLADIAMSKGFAPQVATLDSH----AGNLPREGAVLIV--TASY-NGHPPDNAKQFVDWL
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14.1%; Score 767; DB 6; Length 67
Best Local Similarity 32.4%; Pred. No. 1.3e-57;
Matches 211; Conservative 113; Mismatches 264; Indels
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DATABASE ACCESSION NUMBER: SWISS-Prot / BAB18572
DATABASE ENTRY DATE: 2002-06-15
                                                                                                                                                                                                                                                                 ; Sequence 12757, Application US/10219051B; GENERAL INFORMATION:
                                                                                                                                           1039 GRYAKDVWA 1047
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GRYSLDVWS 682
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ORGANISM: Homo sapiens
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Storen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Sucolated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 70174
LENGTH: 719
                                                                                961 HTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADV 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIIT-L 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 535 SY-NGHPPDNAKQFVDWLDQASADEV--KGVRYSVFGCGDKNWATTYQKVPAFIDETLAA
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                                                                                                                                                              1021 HQVSEADARLWLQQLEEKGRYAKDVW 1046
                                                                                                                                                                                           664 ENVDSSKAEAIVKKLQMDGRYLRDVW 689
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Best Local Similarity
Matches 188; Conserva
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Sequence 187394, Application US/10424599

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8

CURRENT FILING DATE: 2003-04-28

CURRENT FILING DATE: 2003-04-28

SEQ ID NO 187294

LENGTH: 689
                                         RSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAH 995
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VPMFVR--KSQFRLPFKATTPVIMVGPGTGVAPFIGFIQERAWIRQQGKEVGETLLYYGC
                                                               480 TPLLVLYGSNMGTAEGTARDLAD - · IAMSKGFAPQVATLDSHA------GNLPREGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           585 IDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSL
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                                                                                                                         FYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047
                                                                                                                                              73;
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US-10-424-599-187294
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OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Glycine max
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Best Local S
Matches 195
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953 QSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEA 1011
                                                                                                                              765 RAMAAKTVCPPHKVELEALLE----KQAYKEQVLAKRLTMLELLEKYPACEMKFSEFI-AL 820
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 479 FAPQRVHVTCALVYGPTPTG-RIHKGVCSTWMKNAIPLEKSPDCSWAPIFIRPSNFKLPV 537
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                                      DPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENA
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                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tang, Xiao-Song
TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
FILE REPERENCE: BC1009 US DIVCIP
CURRENT APPLICATION NUMBER: US/10/188,523B
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US 09/627,216
PRIOR FILING DATE: 2000-07-27
PRIOR PILING DATE: 1999-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                            RESULT 12
US-10-188-523B-14
; Sequence 14, Application US/10188523B
; GENERAL INFORMATION:
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SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 588
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Best Local Simil
Matches 189;
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APPLICANT: La Rosa Thomas J
APPLICANT: Show Yihua
APPLICANT: Show Yihua
APPLICANT: Can Vongwei
TITLE OF INVENTION: SOy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 191313
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                                                                         962 TAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADVH 1021
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                                                                                               PGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIIT-LH 961
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                                  576 PGTGLAPFRGFLQERLALKQSGAELGTSILFFGCRNRNMDYIYEDELQTFLEEGALSELI
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US-10-424-599-191313
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.larity 28.2%; Pred. No. 1.3e-52;
Conservative 123; Mismatches 288;
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; GENERAL INFORMATION:
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196; Conserv
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US-10-424-599-191313
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18 DLDDYA----ADDEEYAEKFKKETFAFFFLATYGDGEPTDNAARFYKWFTEG---
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                                                    Sequence 14, Application US/10188523C
GENERAL INFORMATION:
APPLICANT: Tang, Xiao-Song
TILE OF INVENTION: BLODRODUCTION OF PARA-HYDROXYCINNAMIC ACID
FILE REFERENCE: BC1009-CIP
CURRENT PAPLICANTION NUMBER: US/10/188,523C
CURRENT FILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 38
SOFTWARE: MICROSOFT OFFICE 97
SEQ ID NO 14
LEMENTH: 588
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; Pred. No. 2.5e-52;
92; Mismatches 245;
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31.9%;
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APPLICANT: Zhou Yihua APPLICANT: Zhou Yihua APPLICANT: Zhou Yihua APPLICANT: Cao Yongwei TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 177338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     984 KKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAK 1043
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US-10-424-599-177338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: unsure at all Xaa locations PERATURE:
                                             Sequence 177338, Application US/10424599
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
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RESULT 14
US-10-424-599-177338
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954 NNSLISNDRSWKRNKFRLTYVAEAPDLTQGLSNVHKRNVSAARLLSRQNLQSPKFSRSTI 1013
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646 SEIWSMISQGAYIYVCGDAKGMARDVHRALHTILQEQGSLDSSKAESMVKNLQTTGRYLR 705
                                                                                                                                                                                                                   APPLICANT: Stuchr, Dennis J.
APPLICANT: Stuchr, Dennis J.
APPLICANT: Stuchr, Dennis J.
APPLICANT: Adak, Subrata
TITLE OF INVENTION: Nucleic Acids Encoding Nitric Oxide Synthase Variants
FILE REFERENCE: 26473/04028
CURRENT APPLICATION NUMBER: US/09/661,258
CURRENT FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        505 MSKGFAPQVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKQF-------
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                                                                                                                                       RESULT 15
US-09-661-258-2
; Sequence 2, Application US/09661258
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-661-258-2
                                        1044 DVW 1046
                                                                     DVW 708
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Search completed: May 29, 2003, 08:26:31 Job time : 58 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: May 29, 2003, 08:26:36; Search time 49 Seconds

(without alignments)
2056.099 Million cell updates/sec
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Title:

US-10-031-146-2

Perfect score:
5457
Sequence:
1 TIKEMPQPKTFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched:
283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:
283224

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR\_73:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		NADPH-ferrihemopro	cytochrome P450 /	NADPH-ferr1hemopro	NADPH-ferrihemopro	protein K10D2.6 [i	nitric-oxide synth																							
SUMMARIES	ID	A34286	D69799	A69975	RDRTO4	RDPGO4	A25505	A60557	S27158	T05582	T14903	A56592	A28577	A47298	T10720	S37159	T14081	T10723	S37157	T14904	S21531	S31502	G88451	156575	JN0609	S16233	S38253	153165	JC5029	G01946
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	Query Match Length	1049	1061	1054	678	677	619	677	678	692	681	671	601	069	683	692	711	705	290	669	712	714	662	1147	1429	1429	1147	1147	1147	1433
de	Query	100.0	60.7	60.1	14.2	14.1	14.1	14.1	14.0	13.6	13.5	13.5	13.2	13.2	13.0	13.0	13.0	12.9	12.9	12.9	12.9	12.9	12.5	12.5	12.4	12.4	12.4	12.4	12.4	12.4
	Score	5457	3314	3281.5	777.5	169	169	167	761.5	739.5	737.5	735.5	723	723	711.5	711	109	206	705.5	705	702.5	702	684.5	683.5	619	678	677.5	675.5	675.5	675
	Result No.	1	7	m	4	ស	Q	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

nitric-oxide synth	NADPH-cytochrome P	nitric-oxide synth	nitric-oxide synth	nitric-oxide synth	NADPH-ferrihemopro	nitric-oxide synth	nitric-oxide synth	NADPH-ferrihemopro	sulfite reductase	sulfite reductase	NADPH-ferrihemopro	NADPH-ferrihemopro	NADPH-ferrihemopro	nitric-oxide synth	nitric-oxide synth
S47647	JE0230	A43271	JC5028	A49676	S38427	JC5027	S65440	863698	A83726	G70040	S63895	S37156	JC7192	T31331	A47501
Н	~	Н	7	7	Н	N	7	7	7	Н	7	7	N	~	н
1147	713	1144	1147	1153	693	1147	1147	680	607	605	089	206	710	1247	1203
12.3	12.3	12.2	12.2	12.1	12.0	12.0	12.0	11.7	11.7	11.5	11.5	11.5	11.3	11.3	11.2
671.5	699	665.5	664.5	661	657.5	654.5	654.5	639	636.5	628.5	628	627.5	617.5	614.5	608.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RAN NO CO	RESULT 1 A34.286 NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - Bacillus megaterium N;Contains: NADPH-ferrihemoprotein reductase (EC 1.6.2.4); unspecific monooxygenase (. C;Species: Bacillus megaterium C;Species: Bacillus megaterium C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002 C;Date: A34.286; S43653
20444	R;Ruettinger, R.T.; Wen, L.P.; Fulco, A.J. J. Biol. Chem. 264, 10987-10995, 1989 A;Title: Coding nucleotide, 5' regulatory, and deduced amino acid sequences of P-450-A;Feference number: A34286; MUID:89291834; PMID:2544578 A;Accession: A34286 A;Molecule type: DNA
4484	A; Residues: 1-1049 <rue> A; Cross-references: GB-J04832; NID:g142797; PIDN:AAA87602.1; PID:g142798 A; Cross-references: GB-J04832; NID:g142797; FIDN:AAA87602.1; PID:g142798 B; Munro, A.W.; Lindsay, J.G.; Coggins, J.R.; Kelly, S.M.; Price, N.C. FEBS Lett. 343, 70-74, 1994 A; Title: Structural and enzymological analysis of the interaction of isolated domains</rue>
ਬੇ ਕੇ ਕੇ ਹੋ	A; Keterence Humber: 543053; MOLD:94415/10; PMID:9103021 A; Mocession: S43653 A; Residues: 430-439;441-496 <mun> C; Genetics:</mun>
4000444	A;Gene: CYP102 G;Superfamily: P450 bifunctional enzyme CYP102; cytochrome P450 homology; flavodoxin C;Scywords: chromoprotein; electron transfer; FAD; flavoprotein; FMN; heme; iron; met F;262-433/Domain: cytochrome P450 homology <p45> F;483-1046/Domain: NADPH-ferrihemoprotein reductase homology <feh> F;485-622/Domain: flavodoxin homology <fen> F;481-622/Domain: flavodoxin homology <fen> F;401/Binding site: heme iron (Cys) (axial ligand) #status predicted</fen></fen></feh></p45>
	Query Match Best Local Similarity 100.0%; Score 5457; DB 1; Length 1049; Best Local Similarity 100.0%; Pred. No. 3.1e-298; Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY Db	1 TIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSGRLIKE 60
Oy Db	61 ACDESRFDKNLSGALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMV 120
QQ Dp	7 121 DIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRA 180 
Q P P	181 LDEAMNKLORANPDDPAYDENKROFOEDIKVMNDLYDKIIADRKASGEQSDDLLTHMLNG 240 111111111111111111111111111111111111

241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVD 300

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R; Kunst, F:; Ogasawara, N:; Moszer, I:; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
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Rleger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadahe, Y.; Sato, T.; Seron
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125 QLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYTRFNSFYRDQPHPFITSMVRALDEA 184	481 PLIVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGAP  485 PLIVLEGSNLGTAEGLAAQGROMGFTAETAPLDDYIGKLPEGGAVLIVTASYNGAP  541 PDNAKOFVDWLDQASADEVKGVRYSVFGCGDKNWATTYGKVPAFIDETLAAKGAENIADR  545 PDNAAGFVEWLEEEGOLKGVSYAVFGCGNSWASTYGKIPRIDDWKARGASKLTAI  601 GEADASDPEGTYEEWREHMWSDVAATFNLDIENSEDNKSTLSLOFVDSAADWLAKMG  1   1   1   1   1   1   1   1   1   1	RESULT 4  RDRNO4  NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - rat  NAAlternate names: NADP-cytochrome P450 reductase  C;Species: Rattus norvegicus (Norway rat)  C;Date: 2.7-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 03-Jun-2002  C;Accession: A36073; A00402; A25813  R;Porter, T.D.; Beck, T.W.; Kasper, C.B.
3		R C C C C C C C C C C C C C C C C C C C
	RESULT 3  NADPH-Ferrihemoprotein reductase (EC 1.6,2.4) - Bacillus subtilis  N. Contains: NADPH-Ferrihemoprotein reductase (EC 1.6.2.4); unspecific monooxygenase (EC 5.26ctess) as Bacillus subtilis  N. Contains: NADPH-Ferrihemoprotein reductase (EC 1.6.2.4); unspecific monooxygenase (EC 5.26ctess) as Bacillus subtilis subtilide, S. Bacillow 1.8 February 1.8 Februar	5 MPOPKTFGELKNLPLINTDKPVQALMKIADELGEIFKFEAPGRVTRXLSSQRLIKEACDE 64 11   :        : :

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cytochrome P-450 reductase from porcin
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sfer; endoplasmic reticulum; FAD; flav
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SVAPFRGFVQARKQLKEQGQSLGEAHLY 933
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SIAPFMGFIQERAWLREQGKEVGETLLY 563
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889 TLFKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEE 948	Db 328 DSALVNQLGEILGADLDVVMSLNNLDEESNKKHPFPCPTSYRTALTYYLDITNPPRTNVL 387
	OY 747 EELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLEKQAYKEQVLAKRLTMLELLEK 806
949 LENAASEGIIT-LHTAFSRMENQP-KTYVQHYMEQDGRKLIELL-DQGAHFYICGDGSQM 1005      - - - - - - - - - - - - - - - - -	Db 388 YELAQYAADPAEQEQLRKMASSSGEGKELYLSWVVEARRHILAILQD 434
	435 YPSLRPPIDHLCELLPRLQARYYSIASSSKVHPNSVHICAVAVEYETKAGRLN-KGVATS
636 ARDVQNTFCDIVAEQGPMEHAQAVDYVKKLMTKGRYSLDVWS 677	QY         867 YL-AELQEGDTITCFISTPQSEFTLEROPETPLIMVGPGTGVAPFRGFVQARKQL         920           :   :  :
RESULT 6 A25505 NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit)	921 KEGGGSLGEAHLYFGCRSPHEDYLYQEELENAGSEGIIT-LHTAFSRMPNQPKTYVOHVM ::  ::     :      :        :  :  :  :  :
C;Date: U3-UcT-1988 #sequence_revision 05-Oct-1988 #text_change 03-Jun-2002, C;Accession: A25505; A05233 F;Katagiri, M.; Murakkmi, H.; Yabusaki, Y.; Sugiyama, T.; Okamoto, M.; Yamano, T.; J. Biochem. 100, 945-954, 1986	ODKAN DD 611 RROKEHLWRLIHEGGAHIYVCGDARNMARDAVEATLMKSYADVHQVSEADARLWLQQLEEK 1038  1
A;Tille: Molecular cloning and sequence analysis of full-length cDNA for rabbit liver A;Reference number: A25505, MUID:87137361; PMID:3029050 A;Accession: A25505 mRNA A;Accession: A25505 mRNA	r NR QY 1039 GRYAKDVWA 1047  Db 671 GRYSLDVWS 679
A.GEOSGUES: 1-6/9 CKATZ. A.GEOSS-references: GBXX04610; NID:91543; PIDN:CAA28279.1; PID:91544 R.Black, S.D.; Coon, M.J.	RESULT 7
J. Biol. Chem. 257, 5929-5938, 1982 A;Title: Structural features of liver microsomal NADPH-cytochrome P-450 reductase. X;Reference number: A05233; MUID:82167456; PMID:6802823	A60557 Hydrc NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - human N;Alternate names: NADP-cytochrome P450 reductase
A; Molecule type: protein A; Molecule type: protein A; Residues: 'PTHDG',14-39,'NY',42-52,'N',54-81 <bla> A; Note: the order of the first four residues was not determined</bla>	C; Species: Homo Sapiens (man) C; Date: 17-Apr-1993 #sequence_revision 31-Dec-1993 #text_change 03-Jun-2002 C; Accession: A33421; A60557; S21686 R; Haniu, M.; McManus, M.E.; Birkett, D.J.; Lee, T.D.; Shively, J.E.
Note: the amino end of the mature protein is acetylated Comment: This enzyme, a membrane-bound flavoprotein containing one molecule each of Fi Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemopri Keywords: acetylated amino end; electron transfer; FAD; flavoprotein; FWN; membrane pr	Blochemistry 28, 8639-8645, 1989 A;Title: Structural and functional analysis of NA;Reference number: A33421; MUID:90105390; PMID: A;Accession: A33421
F.1-56/Domain: membrane-bound #status predicted <mem> 7.8-228/Domain: FMN binding #status predicted <fmn> F.81-677/Domain: NADPH-ferrihemoprotein reductase homology <feh> F.83-225/Domain: flavodoxin homology <fexx></fexx></feh></fmn></mem>	A; Mol A; Res A; Not R: Yan
F;85-96/Region: FMN-phosphate binding #status predicted F;268-327,453-478/Domain: FAD binding #status predicted <fad> F;294-297/Region: FAD-pyrophosphate binding #status predicted</fad>	83-88, 1989 H-P450 oxidoreductase: complementary DNA cloning, sequence and v A60557; MUID:89313720; PMID:2501655
Ouery Match Best Local Similarity 31.7%; Pred. No. 1.9e-35; Matches 212; Conservative 111; Mismatches 250; Indels 96; Gaps 24;	<yam></yam>
444 FUVKAKSKIPLGGIPSPSTEQSAKKVRKKAENAHNTPLLVLYGSNMGTAEGTA 497	R;Shephard, E.A.; Palmer, C.N.A.; Segall, H.J.; Phillips, I.R. Arch. Biochem. Biophys. 294, 168-172, 1992 Aritle: Quantification of cytochrone P450 reductase gene expression in human tissues A;Reference number: S21686; WUID:92198003; PMID:1550342
498 RDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKQFVDW 550	
551 LDQASADEVKGVRYSVFGCGDKNWATIYQKVPAFIDETLAAKGAENIADRGEADASD 607	C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemo C;Keywords: acetylated amino end; electron transfer; endoplasmic reticulum; FAD; flav F;1-56/Domain: membrane-bound #status predicted <mem>F;2-67/Product: NADPH-ferrihemoprotein reductase #status experimental <mat></mat></mem>
608 DFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMH 659	F;77-227/Domain: FMN binding #status predicted <fmn>F;80-675/Domain: NADPH-ferrihemoprotein reductase homology <feh></feh></fmn>

NADPH-ferrihemoin: FMN; NADP; o

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Biochim. Biophys. Acta 1174, 313, 1993
A;Reference number: S38510; MJID:93385164; PMID:8373812
A;Contents: annotation; erratum
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihem
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihem
C;Keywords: electron transfer; endoplasmic reticulum; FAD; flavoprotein; FMN; NADP;
F;79-188/Domain: FMN binding #status predictase homology <FEH>
F;80-676/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;82-224/Domain: flavodoxin homology <FELX>
F;22-326,454-477/Domain: FAD binding #status predicted <FAD>
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A; Residues: 1-692 <BEV>
A; Cross-references: EMBL:AL035356
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                     F:84-95/Region: FMN-phosphate binding #status predicted
F;267-326,452-477/Domain: FMD binding #status predicted <FAD>
F:293-296/Region: FAD-pyrophosphate binding #status predicted
F:2/Modified site: acetylated amino end (Gly) (in mature form) #status experimental
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N;Alternate names: NADPH-cytochrome P450 oxidoreductase
C;Species: Cavia porcellus (guinea pig)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Jun-2002
C;Accession: S27158; S38510
C;Accession: S27158; S38510
C;Accession: S17158; S38510
A;Title: Molecular A; Ishizaki, K.; Kamataki, T.; Shinriki, N.
Biochim. Blophys. Acta 1171, 103-105, 1992
A;Title: Molecular cloning and sequence analysis of mouse NADPH-cytochrome P-450
A;Reference number: S27158; MUID:93041995; PMID:1420354
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                                                                                                                                                                                                                                  444 FVVKAKSKKIP----LGGIPSPSTEQS-AKKVRKKAENAHNTPLLVLYGSNMGTAEGTAR
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                                                                                                                                                14.1%; Score 767; DB 2; Length 677; 32.4%; Pred. No. 2.5e-35;
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                                                                                                       F;566/Binding site: NADP (Cys) #status experimental
                                                                                                                                                                                           Conservative 113; Mismatches
    F;82-224/Domain: flavodoxin homology <FLX>
                                                                                                                                                                     Similarity
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A; Residues: 1-678 <OHG>
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Matches 211;
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NADPH-ferrihemoprotein reductase (EC 1.6.2.4) ATR1 - Arabidopsis thaliana NADPH-ferrihemoprotein reductase (EC 1.6.2.4) ATR1 - Arabidopsis thaliana (Social Social 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           612 TYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMH-------
                                                                                                          Gaps
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     678;
     Length
                                                                                                          Indels
Query Match 14.0%; Score 761.5; DB 2; Best Local Similarity 31.9%; Pred. No. 5e-35; Matches 208; Conservative 111; Mismatches 269;
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A; Gene: CPR
C; Function:
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A; Experimental source: cultivar Columbia; BAC clone F22K18
R; Mignote-Vieux, C.; Kazmaler, M.; Lacroute, F.; Pompon, D.M.
submitted to the EMBL Data Library, May 1992
A; Reference number: $21530
A; Reference number: $21530
A; Molecule type: mRNA
A; Residues: 1-160, S', 162-476, 'CQDW', 481-692 <MIG>
A; Cross-references: EMBL:X66016; NID:q16186; PIDN:CAA46814.1; PID:q16187
C; Genetics:
A; Genetics: 101/3; 121/3; 121/3; 124/3; 207/1; 230/2; 294/2; 325/2; 400/3; 428/3;
A; Map position: 4
A; Introns: 101/3; 121/3; 147/2; 166/3; 194/3; 207/1; 230/2; 294/2; 325/2; 400/3; 428/3;
A; Note: F22K18 _280
C; Superfamily: NADPH-ferrihemoprotein reductase;
C; Superfamily: NADPH-ferrihemoprotein reductase
F; 85-691/Domain: NADPH-ferrihemoprotein reductase
F; 85-691/Domain: NADPH-ferrihemoprotein reductase
F; 85-691/Domain: lavodoxin homology <FEH>
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                                                                                                                                                                                                                                                                                  tch 13.6%; Score 739.5; DB 2; al Similarity 29.6%; Pred. No. 8.9e-34; 196; Conservative 120; Mismatches 257;
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Best Local S:
Matches 196
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A; Description: catalyzes the reduction of the heme-thiolate-dependent monooxygenases; A; Note: expression induced by fungal elicitor-treatment or or UV-irradiation C; Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemo C; Keywords: flavoprotein; NADPH-ferrihemoprotein; F;74-680, Domain: NADPH-ferrihemoprotein reductase homology <FEH>
                                                                                                                                                                        parsley
                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-681 <KOO>
Cross-references: EMBL.AF024634; NID:92809384; PIDN:AAB97736.1; PID:92809385
C;Genetics:
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NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - parsley
NiAlternate names: NADPH 'QYtochrome P450 reductase
C.Species: Petroselinum crispum (parsley)
C.Species: Petroselinum crispum (parsley)
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C.Accession: T14699 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C.Accession: E.; Hahlbrock, K.
Proc. Natl. Acad. Sci. U.S.A. 94, 14954-14959, 1997
A.Title: Differentially regulated NADPH:cytochrome P450 oxidoreductases in pA; Reference number: 218258; MUID:98070859; PMID:9405720
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Pred. No. 1.1e-33;
i; Mismatches 275;
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30.7%;
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Best Local Simil
Matches: 200; C
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Accession: A28577
R; Urenjak, J; Linder, D.; Lumper, L.
J; Chromatogr. 397, 123-136, 1987
J; Chromatogr. 397, 123-136, 1987
J; Chromatogr. 397, 123-136, 1987
J; Chromatogr. 397, 133-136, 1987
J; Title: Structural comparison between the trout and mammalian hydrophilic domain of A; Reference number: A28577; MUID:88008061; PMID:3116019
A; Rolecule type: protein
B; Sesidues: 1-601 cWRE>
C; Superfamily: NADPH-ferrihemoprotein reductase
C; Superfamily: NADPH-ferrihemoprotein reductase
F; 25-599/Domain: NADPH-ferrihemoprotein reductase
F; 27-169/Domain: flavodoxin homology <FLX>
                                                                   C;Species: Salmo trutta (brown trout)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 03-Jun-2002
                                             NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - brown trout (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - mung bean N;Alternate names: NADPH-cytochrome P450 reductase
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                                                                                                       Richard J. F. Carino, F.A.; Feyerelsen, R. Insect Blochem. Mol. Biol. 23, 439-447, 1993
A;Title: The CDNA and deduced protein sequence of house fly NADPH-cytochrome P450 reduct A;Reference number: A56592; MUID:93284260; PMID:8508186
A;Accession: A56592
A;Status: preliminary
A;Residues: 1-671 < KOE>
                                                                                                                                                                                                                                                                        A; Residues: 1-671 <KOE>
A; Residues: 1-671 <KOE>
A; Cross-references: GB:L19897; NID:g308945; PIDN:AAA29295.1; PID:g308946
A; Cross-references: GB:L19897; NID:g308945; PIDN:AAA29295.1; PID:g308946
A; Note: sequence extracted from NCBI backbone (NCBIN:134359, NCBIN:134361, NCBIN:133605, C; Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein; Reyavoratein; membrane protein; NADP; oxidoreductase
F; 77-669/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F: 79-221/Domain: flavodoxin homology <FLX>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Musca domestica (house fly)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|: | : |: || || || || || || XEWITNGEVD-LTGLNYAVFGLGNKTY-EHYNKVAIYVDKRLEELGATRVFELGLGDDDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 MQNQRPPFDAKNPFLASVIVNRELHK-GGGRSCMHIELDIDGSKMRYDAGDHIAMYPIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGIVNRY--TARFGLD-ASQOIRLEAEEEKLAHLP-------LAKTVSVE
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                     reductase
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NAUPH-TETTIHEMOPTOTEIN reductase (EC 1.6.2.4) - house fly N.Alternate names: NADPH-cytochrome P450 reductase; P450
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13.5%; Score 735.5; DB 2;
Best Local Similarity 30.0%; Pred. No. 1.4e-33;
Matches 199; Conservative 123; Mismatches 255;
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                                                                                        459 PSPSTEQSA--KKVRKKAENAHNTPLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATL
                                                                                                                      517 D----SHAGNLPREGAVLIV--TASY-NGHPPDNAKQFVDWLDQASADEVKGVRYSVFGC
                                                                                                                                                                                                         GDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFN
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Length 601;
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                       Best Local Similarity 30.2%; Pred. No. 6.1e-33; Matches 195; Conservative 106; Mismatches 239;
13.2%; Score 723; DB 2; 30.2%; Pred. No. 6.1e-33;
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R;Rosco, A.; Pauli, H.H.; Priesner, W.; Kutchan, T.M.
Arch. Biochem. Blophys. 348, 359-377, 1997
A;Title: Cloning and heterologous expression of NADPH-cytochrome P450 reductases from A;Reference number: Z17096; MUID:98096363; PMID:9434750
A;Reference number: Z17096; MUID:98096363; PMID:9434750
A;Residum T10720
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residumes: 1-683 cROS>
A;Cross-references: EMBL:U67185; NID:g2580496; PIDN:AAC05021.1; PID:g2580497
                                                                                                                                                                                                                                A; Description: catalyzes the reduction of the heme-thiolate-dependent monooxygenases; C; Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemo C; Keywords: flavoprotein; NADPP, oxidoreductase F; 80-682/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F; 80-682/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | :: | | : | | DGS-----PQGSSLPPPFPGPCTLRSALARYADLLNPPRKASLIALSAHASVPSEAERLRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----NLPREGAVLIVTASY-NGHPPDNAKQFVDWLDQ--ASADEVKGVRYSVFGCGDKN
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                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                      atch 13.0%; Score 711.5; DB 2; cal Similarity 30.3%; Pred. No. 3.3e-32; 191; Conservative 113; Mismatches 263;
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Best Local S:
Matches 191,
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C;Species: Vigna radiata (mung bean)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 03-Jun-2002
C;Accession: A47298
R;Shet, M.S.; Sathasivan, K.; Arlotto, M.A.; Mehdy, M.C.; Estabrook, R.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 2890-2884, 1993
A;Title: Purification, characterization, and cDNA cloning of an NADPH-cytochrome P450 re
A;Reference number: A47298; MUID:93219390; PMID:8464904
A;Accession: A47298; MUID:93219390; PMID:8464904
A;Accession: A47299
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-600 cSHE>
A;Experimental source: var. Berken, microsomes
A;Note: sequence extracted from NCBI backbone (NCBIP:128723)
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein; reductase
F;84-233/Domain: flavodoxin homology <FLX>
F;84-233/Domain: flavodoxin homology <FLX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   962 TAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADVH 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - opium poppy
N;Alternate names: ferrihemoprotein P-450 reductase; NADP-cytochrome reductase
C;Species: Papaver somniferum (opium poppy)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
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submitted to the EMBL Data Library, September 1993
X-bescription: Isolation and characterization of a cDNA encoding an NADPH-cytochrome P45
A;Reference number: $37159
A;Accession: $37159
                                                                                                                                                                         A;Cross-references: EMBL:226252; NID:9400531; PIDN:CAA81211.1; PID:9400532
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemopro
C;Keywords: flavoprotein; NADP; oxidoreductase
F;83-691/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;85-234/Domain: flavodoxin homology <FLX>
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A; Molecule type: mRNA
A; Residues: 1-692 <BEN>
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Search completed: May 29, 2003, 08:31:43 Job time : 52 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

May 29, 2003, 08:22:51 ; Search time 26 Seconds (without alignments) 1671.815 Million cell updates/sec

US-10-031-146-2 5457 1 TIKEMPQPKTFGELKNLPLL.....RLWLQQLEEKGRYAKDVWAG 1048 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 ; Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	<b>⊶</b>	79	008394 bacillus su	008336 bacillus su	P37040 mus musculu	P00388 rattus norv	P04175 sus scrofa	P00389 oryctolagus	P16435 homo sapien	P37039 cavia porce	Q07994 musca domes				_	Q06518 rattus norv	Q9z0j4 mus musculu	w	5 homo	homod	mus m			Q90703 gallus gall		Q26240 rhodnius pr		O61608 anopheles s	P29474 homo sapien	m	P70313 mus musculu	Q28969 sus scrofa		Q27571 drosophila
SUMMARIES	. OI	CPXB_BACME	CYPD_BACSU	CYPE_BACSU	NCPR_MOUSE	NCPR_RAT	NCPR_PIG	NCPR_RABIT	NCPR_HUMAN	NCPR_CAVPO	NCPR_MUSDO	NCPR_DROME	NCPR_SALTR	NCPR_PHAAU	NCPR_CATRO	NOS2_RAT	NOS1_MOUSE	NOS1_RAT	NOS1_HUMAN	NS2D_HUMAN	NOS2_MOUSE	NOS1_RABIT	NS2A_HUMAN	NOS2_CHICK	NOS2_CAVPO	NOS_RHOPR	NCPR_CANMA	NOS_ANOST	NOS3_HUMAN	NOS3_BOVIN	NOS3_MOUSE	NOS3_PIG	~	NOS_DROME
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FIRE COON	NCPR_SCHPO	MTRR_HUMAN	NCPR YEAST	CYSJ_ECOLI	NOS_LYMST	CYSJ_SALTY	CYSJ_BUCAI	NOS3_RAT	MTRR_CAEEL	C972_SOYBN	C973_ARATH	
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401	678	725	9	598	1153	598	601	919	682	576	580	,
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3.4	32	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
"Pivotal role of water in the mechanism of P450BM-3.";
Bjochemistry 40:13456-13465(2001).
-!- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. CATALYSES
HYDROXYLAATION OF MEDIUM AND LONG-CHAIN FATTY ACIDS AT OMEGA-1,
OMEGA-2 AND OMEGA-3 POSITIONS, WITH OPTIMUM CHAIN LENGTHS OF 14-16
CARBONS (LAURIC, MYRISTIC, AND PALMITIC ACIDS). THE REDUCTASE
DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
                                                                                          oxidized flavoprotein + H(2)0.
COFACTOR: FAD AND FNN.
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00371; FPNCR.
PRINTS; PR00371; FPNCR.
PROSITE; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme; Multifunctional enzyme; FMN; FAD; Flavoprotein; 3D-structure; NADP.
DOMAIN 1 471 CXTOCHROME P450.
BINDING 400 400 HEME.
                                                                   CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
                                                                             ferrocytochrome.
CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH
                                                                                                                                                                                                                                                                             InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR001099; FAD_binding.
InterPro; IPR001709; FNL_Cyt_redetse.
InterPro; IPR001226; Flavodoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00067; P450; 1.
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00175; NAD_binding; 1.
                                                                                                                                                                                                      EMBL; J04832; AAA87602.1; -
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PDB; 1BU7; 23-SEP-98.
PDB; 1BVY; 23-FEB-99.
PDB; 1JPZ; 09-NOV-01.
                                                                                                                                                                                                                      2HPD; 31-OCT-93.
2BMH; 31-JUL-94.
1FAG; 12-FEB-97.
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Pred. No: 9e-298;
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Best Local Similarity 100.
Matches 1048; Conservative
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                                                      GEADASODFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMHG
                                                                                     AFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL
                                                                                                                    BALLEKQAYKEQVLAKRLIMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEK
                                                                                                                                                                                QASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIM
                                                                                                                                                                                                                VGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIARE 97453479; PubMed=9308178;
Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J.,
Duesterhoeft A., Ehrlich S.D.;
"Sequence of the Bacillus subtilis genome region in the vicinity of
the lev operon reveals two new extracytoplasmic function RNA
polymerase signa factors Sigv and Sig2.";
                                                                                                                                                                                                                                                                                                                                                                                                          P450 reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable bifunctional P-450 NADPH-P450 reductase 1 [Includes: Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase 1 [Includes: Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase [EC 1.6.2.4]].
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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                                                                                                                                                                                                                                                                                                              HQVSEADARLWLQQLEEKGRYAKDVWAG 1048
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                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                          CYPD OR CYP102A2
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Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connecton I.F., Cummings N.J., Daniel R.A., Choi S.K., Codani J.J., Connecton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., R. Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Farington J., Fabret C., Ferrari E., Foulger D., R. Fritz C., Fujita M., Fujita Y., Fuma S., Galightly E.J., Grandi G., R. Halbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., B. Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., R. Hulta B., Koadyashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Kobayashi Y., Levine A., Liu H., Masuda S., Mauel C., Medique C., R., Medina N., Mellado R.P., Mizuno M., Mesell D., Nakai S., Nadack M., R., Dohi T.W., Portetelle D., Porvolit S., Prescott A.M., Parsecan E., Pulic P., Purnelle B., Ropoport G., Rey Bark S.H., R. Farsecan E., Scanlan E., Schleich S., Schroeter R., Scoffone F., R. Sekjuchi J., Sekowska A., Seroc S.J., Serror P., Shin B.S., Soldo B., Schroeter R., Kaeuchi M., Tamakashi H., Takamaru K., Vasalotti A., Tanaka T., Takahashi H., Takemaru K., Vasalotti A., Tanaka T., Terpstra P., Tognon A., Yanakeohi M., Wanler F., Vasarotti A., Yanamanoto H., Vanner F., Vasarotti A., Yanamanoto H., Vanner F., Vasarotti A., Yanamanoto H., Yanane K., Yasanotti A., Yanamanoto H., Yanane K., Yasanotti A., Yanane S., Waldeler E., Wedler E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ferrocytochrome.
--- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH + oxidized flavoprotein + H(2)0.
---- COFACTOR: FAD AND FWN (By similarity).
---- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
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Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP;
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NADPH-P-450 REDUCTASE.
HEME (BY SIMILARITY).
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InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001226; Flavodoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00175; NAD_binding; 1.
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PRINTS; PR00371; FPNCR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P450 (BY SIMILARITY).
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1061 AA;
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Length 1061;

DB 1;

Score 3314;

60.78;

1026 QKAYQAVHGTGEQEAQNWLRHLQDTGMYAKDVWAG 1060

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SEGIITLHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATL 1013
                                                                                                                                                                                                                                                                                                                                                        535
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                                                                                                                                                    MNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSD-DLLTHMLNGKDP 243
                                                                                                                                                                                            303
                                                                                                                                                                                                     SYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDELMVLIPQLHRD 363
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                                                                                                            QLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRALDEA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TARFGLDASQQIRLEAEEEKLAHLPLAKTVSVEELLQY-VELQDPVTRTQLRAMAAKTVC 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQ 953
                                                99
                                        5 MPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKEACDE
                                                                                                                                                              EDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGIPSPSTEQSA---KKVRKKAENA---
                                                                                                                                                                                                                                                                                                                                                        --HNTPLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVDPVP
                                                                                                                                                                                                                                                                          KTIWGDDVEEFRPERFENPSAIPQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKHFDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAKMHGAFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDIITCFISTPQSEFTLPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                    596 NIADRGEADASDDFEGTYEEWREHMWSDVAAYFNLDI-ENSEDNKSTLSLQFVDSAADMP
            Gaps
          12;
          Indels
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 Pred. No. 7.1e-178;
          Mismatches
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         Conservative 156;
59.5%;
 Similarity
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RAK KUNST E., Oggsawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Brusshi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brusshi C.V., Candwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brish C.V., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Britz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghims S.Y., Claser P., Goffeau A., Golightly B.J., Grandi G.,
A Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kubia K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Kutia K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Media N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Robayashi Y., Roetter P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Robayashi Y., Scallul B., Roche B., Rose M., Sadaie Y.,
RA Rober B., Pull T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Researa E., Puljic P., Purnelle B., Roche B., Rose M., Sadaie Y.,
Schiuchi J., Sckowska A., Seros S.J., Serror P., Shin B.S., Soldo B.,
Sckiguchi J., Sckowska A., Seros S.J., Serror P., Shin B.S.,
Sorokin A., Tacconi E., Takagi T., Tarkahashi H., Tarkemaru K.,
RA Takeuchi M., Tamakoshi A., Tanamotol M., Vannier F., Vassarotti A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Tosato V., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Winpat A., Yamamoto Of H., Yamane K., Yasumoto K., Yata K.,
The complete genome sequence of the Gram-positive bacterium Bacillus
F. F. Free F.
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-1- CORACTOR: FAD AND FMN (By similarity).
-1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NATURE 390:249-256(1997).
-!- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE
DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
                                                                                                                                                       16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable bifunctional P-450:NADPH-P450 reductase 2 [Includes:
Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in the vicinity of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97453479; PubMed-9308178; Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J., Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J., Duesterhoeft A., Ehrlich S.D.; Sequence of the Bacillus subtilis genome region in the vicir the lev operon reveals two new extracytoplasmic function RNA polymerase sign factors SigV and SigZ."; Microbiology 143:2939-2943(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome
                                          1054 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98044033; PubMed-9384377;
                                                                                                                 (Rel. 40, Created)
                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P450 (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                      CYPE OR CYP102A3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                (EC 1.6.2.4)
                                                                                                                      16-OCT-2001
                                     CYPE_BACSU
008336;
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CYPE_BACSU
                                                                                DDT TO THE SECOND OF SECON
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FROM N.A.
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P37040;
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STRAIN-ddY;
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NCPR_MOUSE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQS-DDLLTHMLNGKDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGIPSPSTEQS---AKKVRKKAENAHNT
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                                                                                                                                                                                                                                                                                    Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme; Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP;
                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1054;
                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                            HEME (BY SIMILARITY).
fW; 705F8E27866Call0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                  NADPH-P-450 REDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 60.1%; Score 3281.5; DB 1; Best Local Similarity 58.5%; Pred. No. 4.6e-176; Matches 614; Conservative 173; Mismatches 254;
                                                                                                                                                                                                                                                                                                                       CYTOCHROME P450
                                                                                                                          Subtilist; BG12299; cypE.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR001097; FAD_binding.
InterPro; IPR001209; FPN_cyt_redctse.
InterPro; IPR001226; Plavodoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00175; NAD_binding; I.
Pfam; PF00258; flavodoxin; I.
Pfam; PF00657; FAD_binding; I.
                                                                                                                                                                                                                                                                       PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                         118675 MW;
                                                                                      U93874; AAB80867.1; -.
                                                                                                      Z99117; CAB14658.1;
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PR00385; P450.
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1054 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                          AFSTNVVASKELQQPGSARSTRHLEIELPKEASYQEGDHLGVIPRNYEGIVNRVTARFGL
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                                                             NADP
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"Mouse NaDPH-cytochrome P-450 oxidoreductase: molecular cloning and functional expression in yeast.";
Biochim. Biophys. Acta 1186:137-141(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
SIMILARITY: THE FWN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOWOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
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ROVIDE ELECTRON
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Last annotation update)
reductase (EC 1.6.2.4) (CPR) (P450R)
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e by non-profit institutions as long as its content is in no way failied and this statement is not removed. Usage by and for commercial tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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PRINTS; PRO0371; FPNCN.
Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum; Membrane; Acetylation.
                                                                                                                                                                                                                                                                                                              ACETILATION (BY SIMILARITY).
FEMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
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InterPro; IPR001097; FAD_binding.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001709; Flavodoxin_like.
InterPro; IPR00126; Flavodoxin_like.
InterPro; IPR00143; Oxred_FAD/NAD(P).
Pfam; PF000175; NAD_binding; 1.
Pfam; PF00667; FAD_binding; 1.
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32.3%;
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677 AA;
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SEQUENCE
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993 -GAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.80 ANGSTROMS) OF MUTANTS.
MEDLINE-21369908; PubMed=11371558;
Hubbard P.A., Shen A.L., Paschke R., Kasper C.B., Kim J.-J.P.;
"NADPH-cytochrome 4450 oxidoreductase. Structural basis for hydride
                                                                                                                                                                                                                                                                                                                                                                                                                                                                domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
-i- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and electron transfer.";
J. Biol. Chem. 276:29163-29170(2001).

J. Biol. Chem. 276:29163-29170(2001).

TO CYTOCHON: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NP.

TO CYTOCHROME P450. IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.

-1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
                    'Three-dimensional structure of NADPH-cytochrome P450 reductase:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang M., Roberts D.L., Paschke R., Shea T.M., Masters B.S.S., Kim J.-J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MUTABALI H., Yabusaki Y., Ohkawa H.;
Murakami H., Yabusaki Y., Ohkawa H.;
"Expression of rat NADPH-cytochrome P-450 reductase cDNA in Saccharomyces cerevisiae.";
                                                                                                                                                                             21.JUL-11986 (Rel. 01, Created)
1-JUR-1993 (Rel. 25, Last sequence update)
15.JUN-2002 (Rel. 41, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
                                                                                                                                                                                                                                                                                                                                                                                                                      Porter T.D., Kasper C.B.;
"Coding nucleotide sequence of rat NADPH-cytochrome P-450 oxidoreductaes CDNA and identification of flavin-binding of Proc. Natl. Acad. Sci. U.S.A. 82:973-977(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prototype for FMN- and FAD-containing enzymes."; Proc. Natl. Acad. Sci. U.S.A. 94:8411-8416(1997).
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                                                                                                                                        677
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MEDLINE-97385116; Pubmed-9237990;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-85140278; PubMed=3919392;
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    1 - COFACTOR: FAD AND FMN.

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                                                                                                                                                                                                                                                                                                           -GAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047
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MEDLINE-87075664; PubMed-3098240;
WOGGI F., Lumpher L.;
"Complete structure of the hydrophilic domain in the porcine NADPH-cytochrome P-450 reductase.";
Blochem. J. 236:81-878(1986).

-1 FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME P-450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
                                                                ---ITCFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLY
                                                                                                                          505 RALVPMFVR--KSQFRLPFKSTTPVIMVGPGTGIAPFMGFIQERAWLREQGKEVGETLLY
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-!- SUBCELLULM AND ALCAPION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
-!- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE REDUCTASE.
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Complete amino acid sequence of NADPH-cytochrome P-450 reductase
from porcine hepatic microsomes.";
Biochemistry 25:7906-7911(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome - NADP(+) + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Amborn J., Preliss B., Stender B., Viale M., Repp R.Z., Lampert
Kroger M., Lumper L.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-1987 (Rel. 04, Created)
Ol-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBL_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            677 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L33893; AAA85368.1; -.
PIR; A00403; RDPGO4.
PIR; A25584; A25584.
HSSP; P16435; 1B1C.
InterPro; IPR003097; FAD_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-87101085; PubMed-3099837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1 - COFACTOR: FAD AND FMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ferrocytochrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                scrofa (Pig)
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SEQUENCE.
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NCPR_PIG
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                         lities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
   and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 RLSKDAHRYGMRGMSADPEEYDLADLSSLPEIDKSLVVFCMATYGEGDPTDNAQDFYDWL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGIVNRVTARFG--LDASQQIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLR 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327 SALVNQIGEILGADLDVIMSLNNIDEESNKKHPFPCPTTYRTALTYYLDITNP-PRTNVL 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              386 YELAQYASEPSEQEHLHKMASSSGEGKELYLSWVVEARRHILAILQDYPSLRPPIDHLCE 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   444 FVVKAKSKKIP----LGGIPSPSTEQS-AKKVRKKAENAHNTPLLVLYGSNMGTAEGTAR 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  552 DQASADEVKGVRYSVFGCGDKNWATTYQKVPA---FIDETLAAKGAENIADRGEADASDD 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLADIAMSKGFAPQVATLDSH----AGNLPR--EGAVLIVTASY-NGHPPDNAKQFVDWL 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.

ACETYLATION (BY SIMILARITY).

FWN (PYRINDINE PART) (BY SIMILARITY).

FAD (ADP PART) (BY SIMILARITY).

FAD (FLAVIN PART) (BY SIMILARITY).

NADP (RIBOSE PART) (BY SIMILARITY).

NADP (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : || | | : || : || : | : | : | : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         509 FEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --------GAFSTNVVASKELQQPGSARSTRHLEIEL-PKEASYQEGDHLGVIPRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tch 14.2%; Score 777.5; DB 1; Length 677; al Similarity 32.2%; Pred. No. 3e-36; 211; Conservative 111; Mismatches 263; Indels 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> A (IN REF. 3).
A957C40E7CEB8F81 CRC64;
   this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003097; FAD_binding.
InterPro; IPR001709; FPM_cyt_redctse.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001024; Flavdoxin_like.
InterPro; IPR001433; Oxrad_FAD/NAD(P).
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00558; flavdoxin; 1.
Pram; PR00667; FAD_binding; 1.
PRINTS; PR00579; FLAVDOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3D-structure.
                                                                                                                                                                                                                                              M58933; AAA41683.1; JOINED.
M58934; AAA41683.1; JOINED.
M58935; AAA41683.1; JOINED.
M58936; AAA41683.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 v
76831 MW;
                                                                                                                       EMBL; M10068; AAA41064.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                           PDB; 1J9Z; 22-AUG-01.
PDB; 1JA0; 22-AUG-01.
PDB; 1JA1; 22-AUG-01.
                                                                                                                                                                                                                                                                                                                                                                                              1AMO; 17-JUN-98
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313
450
529
624
254
677 AA;
                                                                                                                                                                                                                 M58932;
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MOD_RES
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-+ Local '
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : |: | | | : : : | | | : : : | | | : : : | | : | | : : : | | | : : : | | DIVMSLNNLDEESNKRHPFPCPTTYRT-ALTYYLDITNPPRTNVLYELAQYASEPSEQEQ 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKVHPNSVHICAVVVEYETKSGRVN-KGVATSWLRAKEPAGENGRRALVPMFVR--KSQF
                                                                                                                                                                                                                                                                                                                                                                                                                       SERVALESATDMVLFSLIVGLLTYWFIFRKKXDEVPEFSKIETTTSSVKDSSFV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 KKIPLGGIPSPSTEQSAKKVRKKAENAHNTPLLVLYGSNMGTAEGTARDLADIAMSKGFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     511 PQVATLD----SHAGNLPR-EGAVLI-VTASY-NGHPPDNAKQFVDWLDQASADEVKGVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YSVFGCGDKNWATTYQKVPA---FIDETLAAKGAENIADRGEADASDDFEGTYEEWREHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----DMPLAKMHGAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNVVASKELQQPGSARSTRHLEIEL-PKEASYQEGDHLGVIPRNYEGIVNRVTARFGLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             723 SQQI---RLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAAKTVCPPHKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         835 PRVDEKQASITVSVVSGEAWSGYGEYKGIASNYL-AELQEGDT----ITCFISTPQSEF
                                                                                                                                                                                                                                                                                                                                                                                                         401 IGQQFALHEAT-----LVLGMMLKHFDFEDHTNY--ELDIKETLT--LKPEGFVVKAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPAVCEHFGVEATGEESSIRQYELVVHTDMDTAVVYTGEMGRLKSYENQKPFFDAKNPFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEALLE-----KQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYSISSS
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001205; Flavddxin_like.
InterPro; IPR001225; Flavddxin_like.
InterPro; IPR001255; Flavddoxin.
InterPro; IPR001433; Oxred_FBD/NAD(P).
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00559; FIAvodoxin; 1.
PRINTS; PR00569; FLAVODXIN.
PRINTS; PR00369; FLAVODXIN.
PRINTS; PR00371; FPNCR.
Membrane; Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                             ACETYLATION (BY SIMILARITY).
FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                    94;
                                                                                                                                                                                                                                                                                                                                                              Length 677;
                                                                                                                                                                                                                                                                                                                                                                                    275; Indels
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                                                                                                                                                                                                                                                                                                                                     26073A0B97EE3DFF CRC64;
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                                                                                                                                                                                                                                                                                                                                                             14.1%; Score 769; DB 1; 31.9%; Pred. No. 8.9e-36;
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                                           NADP
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-i- SIMILARITY: THE FWN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
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J. Biol. Chem. 257:5929-5938(1982).
-1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NATIO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
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Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Katagiri M., Murakami H., Yabusaki Y., Sugiyama T., Okamoto M., Yamano T., Ohkawa H.; "Molecular clonning and sequence analysis of full-length cDNA for rabbit liver NADPH-cytochrome P-450 reductase mRNA."; J. Biochem. 100:945-954(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Black S.D., Coon M.J.; "Structural features of liver microsomal NADPH-cytochrome P-450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
1-JUL-19966 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
                                                                                                                                       1006 APAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047
                                                                                                                                                                               ARDVQNTFCDIVAEQGPMEHAQAVDYVKKLMTKGRYSLDVWS 677
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InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001226; Flavcdoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P).
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PIR; A05233; A05233.
HSSP; P16435; IBIC.
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                                                                                                                                                               RDLADIAMSKGFAPQVATLDSH----AGNLPREGAVLIV--TASY-NGHPPDNAKQFVDW
                                                                                                                                                                                              LDQASADEVKGVRYSVFGCGDKNWATTYQKVPA---FIDETLAAKGAENIADRGEADASD
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                                                     FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (ELAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
W -> NY (IN REF. 2).
E -> N (IN REF. 2).
                                                                                                                                         Gaps
Pfam; PF00258; flavodoxin; 1.
Pfam; PF00667; FAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavorotein; FMN; FAD; NADP; Endoplasmic reticulum; Membrane; Acetylation.
                                                                                                                                         96;
                                                                                                                        Length 679;
                                                                                                                                        Conservative 111; Mismatches 250; Indels
                                                                                                                        Score 769; DB 1;
Pred. No. 8.9e-36;
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31.78;
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MEDLINE-99156068; PubMed-10048323;
Zhao G., Modl S., Smith G., Paine M., McDonagh P.D., Wolf C.R.,
Tew D., Lian L.Y., Roberts G.C., Driessen H.P.;
"Crystal structure of the FMN-binding domain of human cytochrome P450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shephard E.A., Palmer C.N., Segall H.J., Phillips I.R.; "Quantification of cytochrome P450 reductase gene expression in human
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-!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
-!- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAN DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
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                                                                                                                                                                                                                       Euteleostomi;
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MEDILE-90105300; PubMed-2513880;
MEDILE-90105300; PubMed-2513880;
MEDILE-90105300; PubMed-2513880;
Structural and functional analysis of NADPH-cytochrome P-450 reductase from human liver: complete sequence of human enzyme NADPH-binding sites,";
Biochemistry 28:8639-8645(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murakami H.O., Ogawa H., Nisimoto Y.; "CDNA cloning and characterization of NADPH-cytochrome P-450 in human HL-60 cell."; Che EMBL/GenBank/DDBJ databases.
                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butel:
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
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"Polymorphism of human CYPOR: expression of new allele."
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                              01-AUG-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR)
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Protein Sci. 8:298-306(1999).
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MEDLINE-92198003; PubMed-1550342;
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   Created)
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(Rel. 15,
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NCBI_TaxID-10141;
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313
450
529
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                                                           NCPR_CAVPO
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MOD_RES
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                                                  NCPR_CAVPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAH 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRSDEDYLYREELAQFHRDGALTQLNVAFSREQSH-KVYVQHLLKQDREHLWKLIEGGAH 624
                                                                                                                                                                                                                                                                                                                                          95
                                                                                                                                                                                                                                                                                                                                                                                                               GETDVD-LSGVKFAVFGLGNK----TYEHFNAMGKYVDKRLEQLGAQRIFELGLGDDDGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 LEEDFITWREQFWPAVCEHFGVEATGEESSIRQYELVVHTDIDAAKVYMGEMGRLKSYEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLADIAMSKGFAPQVATLDSH----AGNLPREGAVLIV--TASY-NGHPPDNAKQFVDWL
                                                                                                                                                                                                                                                                                                                                                                          DQASADEVKGVRYSVFGCGDKNWATTYQKVPA---FIDETLAAKGAENIADRGEADASDD
                                                                                                                                                                                                                                                                                                                                                                                                                                          FEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQF---VDSA----ADMPLAKMH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GAFSTNVVASKELQQPGSARSTRHLEIEL-PKEASYQEGDHLGVIPRNYEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271 QKPPFDAKNPFLAAVTINRKLNQ-GTERHLMHLELDISDSKIRYESGDHVAVYPANDSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VNRVTARFG - - LDASQQIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKTVCPPHKVELEALLE-----KQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITCFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGC
                                                                                                                                                                                                                                                                                                                       FVVKAKSKKIP----LGGIPSPSTEQS-AKKVRKKAENAHNTPLLVLYGSNMGTAEGTAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIRPRYYSISSSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYL-AELQEGDT----
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                   Endoplasmic reticulum;
                                                                                                                                       FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047
                                                                                                                                                                                                                                                                                                    64;
                                                                                                                                                                                                                                                                               Score 767; DB 1; Length 676;
Pred. No. 1.1e-35;
                                                                                                                                                                                                                                                                                                   Conservative 113; Mismatches 264; Indels
                                                                                                                                                                                                                               M -> L (IN REF. 4).
F -> L (IN REF. 2 AND 4).
                                                                                                                                                                                                                                                            883EA13797020D70 CRC64;
                                                                                                             Polymorphism; 3D-structure.
                                                                                                                                                                                                                                                  (IN REF.
                                                                                                                                                                                        A -> V.
/FTId=VAR_004617.
R -> Q.
                                                                                                   NADP;
                                                                                                                                                                                                                     /FTId-VAR_004618
       InterPro; IPR001709; FPN_CYL_redetse.
InterPro; IPR0011094; FPN_CYL_redetse.
InterPro; IPR0011094; FPN_CYL_redetse.
InterPro; IPR001205; FNAvodoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PP00175; NAD_binding; 1.
Pfam; PF000258; flavodoxin; 1.
Pfam; PF000578; FAD_binding; 1.
PRINTS; PR00376; FLAVODOXIN.
PRINTS; PR00376; FPNCR.
PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; FMN; FAD; NA
Membrane; Acetylation; Polymorphism; 3D-sf
                                                                                                                               ACETYLATION
                                                                                                                                                                                                                                                                               14.18; Score 767;
                                                                                                   FAD;
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                                                                                                                                                                                                                                                            76558 MW;
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324
460
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313
450
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517
536
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CONFLICT
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i - CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO ORIGINATE FROM MOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FMN; FAD; NADP; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.

ACETYLATION (BY SIMILARITY).
FWN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBCELLUIAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
-i- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-93385164; PubMed-8373812;
MEDLINE-97385164; PubMed-8373812;
Modylya S., Goda T., Ishlazaki K., Kamataki T., Shinriki N.;
Biochim. Biophys. Acta 1174:313-313(1993).
-i- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NATO CYTOCHROME A450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEMP OXYGENASE AND CYTOCHROME B5.
-i- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome - NADP(+) + 2
                                    9/9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Hartley;
MEDLINE-93041955; PubMed-1420354;
OHGIVA S., Goda T., Ishizaki K., Kamataki T., Shinriki N.;
"Molecular cloning and sequence analysis of guinea-pig NADPH-cytochrome P-450 oxidoreductase.";
                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
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InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001226; Flavodoxin.
                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00175; NAD_binding; 1.
Pfam; PF00258; flavodoxin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D10498; BAA01385.1; -.
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HSSP; P00388; 1AMO
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                                                                             444 FVVKAKSKKIP----LGGIPSPSTEQS-AKKVRKKAENAHNTPLLVLYGSNMGTAEGTAR
                                                                                               FLFRKKKEEIPEFTKISTTTSSVKESSFVEKMKKTGRN----IIVFYGSQTGTAEEFAN
                                                                                                                       DLADIAMSKGFAPQVATLDSH----AGNLPR--EGAVLIVTASY-NGHPPDNAKQFVDWL
                                                                                                                                      DQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDDFEG
                                                                                                                                                                                        156 QETDLD-LSGVKYAVFGLGNKTY-EHFNSMGKYVDQRLEQLGAQRIFELGLGDDDGNLEE
                                                                                                                                                                                                                                  DFITWREQFWPAVCEFFGVEATGEESSIRQYELVL---HADTDPAKVYTGEMGRLKSYEN
                                                                                                                                                                                                                                                         -----GAFSTNVVASKELQQPGSARSTRHLEIEL-PKEASYQEGDHLGVIPRNYEGI
                                                                                                                                                                                                                                                                       271 QKPPFDAKNPFLAAVTTNRKLNQ-GTERHLMHLELDISDSKIRYESGDHVAVYPANDSNL
                                                                                                                                                                                                                                                                                                      VNRVTARFG -- LDASQQIRLEAEEEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMA
                                                                                                                                                                                                                                                                                                                          330 VNOLGKILGADLDVVMSLKNLDEESNKKHPFPCPTTYRTALTYYLDITNP-PRTNVLYEL
                                                                                                                                                                                                                                                                                                                                                 AKTVCPP-----HKVELEALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLP
                                                                                                                                                                                                                                                                                                                                                               SIRPRYYSISSSPRVDEKQASIIVSVVSGEAWSGYGEYKGIASNYL-AELQEGDT----
                                                                                                                                                                                                                                                                                                                                                                                                          RSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNOPKTYVQHVMEQDGKKLIELL-DQGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRSDEDYLYREELAQFHKDGTLTQLNVAFSREQAQ-KVYVQHLLKRDQEHLWKLIHEDGA
                                                                                                                                                                                                              TYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLAKMH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koener J.F., Carino F.A., Feyereisen R.; "The cDNA and deduced protein sequence of house fly NADPH-cytochrome P450 reductase.";
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pancrustacea; Hexapoda;
Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65;
ADP (ADP PART) (BY SIMILARITY) 4CA758F28EB84938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-00T-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
                                                         Indels
                                                      208; Conservative 111; Mismatches 269;
                                Score 761.5; DB 1
Pred. No. 2.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthrópoda; Mandibulata;
Insecta; Pterygota; Neoptera; Endopterygota;
Muscomorpha; Muscoidea; Musca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insect Biochem. Mol. Biol. 23:439-447(1993).
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 NADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-Rutgers; TISSUE-Abdomen;
MEDLINE-93284260; Pubmed-8508186;
          76650 MW;
                                14.0%;
31.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Musca domestica (House fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
          677 AA;
                                             Similarity
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AC 007994;
DT 01-0CT-1994
DT 01-0CT-1994
DT 16-0CT-2001
DE NADPH-CYTCOTH
OS MUSCA GOMEST
OC EUKATYOCA: M
OC INSECTA: PER
OC MUSCOMOTIPA;
OX NCBL_TAXID-7
RN | 1]
RP SEQUENCE FRC STRAIN-RUSGS
RX MEDLINE-9328
RA KOENET J.F.;
RA The CDNA an RT The CDNA an RT Insect Bloch
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
                                                                                                                        -1 COFACTOR: FAD AND FMN.
-1 - SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY 1TS N-TERMINAL HYDROPHOBIC REGION.
-1 - DEVELOPMENTAL STRAGE: EXPRESSED THROUGHOUT DEVELOPMENT, WITH HIGH LEVELS BEFORE METAMORPHOSIS AND LOW LEVELS IN PUPAE.
-1 - SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADPAR REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
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                      TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FMN (PYRIMIDINE PART) (BY SIMILARITY FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
A00A2C35DFD8D129 CRC64;
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                                                                              CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+)
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Pred. No. 6.6e-34;
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InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR0010226; Flavdoxin_like.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00275; Flavdoxin; 1.
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InterPro; IPR001709; FPN_cyt_redc
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30.0%;
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ELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLEKQAYKEQVLAKRLTMLELLEKY 807

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RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holf R.A.,
Ranatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewils S.E., Kichards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewils S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Bazer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Berman B.P., Bradari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Cabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
                                                                                                                                                                                                                                                                                                         KLIELL-DQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAK 1043
|| :| | : || || : || || ELAEY---GKEKYQNWIQNSSRNIVHILEDI 431
                                                                                   LAELQE--GDT-ITCFISTPQSEFTLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQG 924
                                                                                                                                                                                                                        QSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIITLHTAFSRMPNQPKTYVQHVMEQDGK 984
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                                                                                                                                                              808 PACEMKFSEFIALLPSIRPRYYSISSSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNY
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Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
STRAIN-Canton-S; TISSUE-Antenna;
MEDLINE-97311413; PubMed-9168130;
Hovemann B.T., Seblmeyer F., Malz J.;
"Drosophila melanogaster NADPH-cytochrome P450 oxidoreductase:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCPR_DROME STANDARD; PRT; 679 AA. 027597; O9VMF2; C=0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) 16-0CT-2001 (Rel. 40, Last annotation update) NADPH-CYLOChrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Berkeley;
MEDLINE-20196006; PubMed-10731132;
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RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.E.,

RA Melson D.R., Nixon K., Musskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Rathert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Spier E., Siden Kiamos I., Simpson M., Skrops M. B., Smith T.,

RA Spier E., Spradiing A.C., Stapleton M., Skrops R., Sun E.,

RA Stirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Then S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Then S.M., Myers E.W., Rubin G.M., Venter J.C.;

The genome sequence of Drosophila melanogaster.";

Science 287.2185-2195(2000).

TO CYTOCHROME 450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON

TO CYTOCHROME 450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON

TRANSFER TO HEME OXYGENASE AND CYTOCHROME B. MAY FUNCTION TO

CC TEARR THE OLIPACTORY ORGAN (ANTENNEE) FROM ACCUMULATING CHEMICALS.

C. -- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome - NADP(+) + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION (BY SIMILARITY).
-i- TISSUE SPECIFICITY: HIGH IN ANTENNAE.
-i- DEVELOPMENTAL STAGE: EMBRYOS AND ADULITS.
-i- SIMILARITY: THE FMN-SINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYIOCHROME B5 REDUCTASE, AND GLUTATHIONE
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Pfam; PF00558; FAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
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FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
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NADP (ADP PART) (BY SIMILAR,
AA -> VT (IN REF. 1).
S -> T (IN REF. 1).
I -> T (IN REF. 1).
I -> T (IN REF. 1).
W; C6387C111A0EDB4A CRC64;
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Best Local Similarity 29.8%; Pred. No. 2.4e-33;
Matches 191; Conservative 113; Mismatches 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P16435; 1B1C.
FlyBase; FBGN0015623; Cpr.
InterPro; IPR003097; FAD_binding.
InterPro; IPR001709; FPN_Cyt_redctse.
InterPro; IPR0011094; Flavdoxin_like.
InterPro; IPR001226; Flavdoxin_like.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00175; NAD_binding; 1.
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331
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555
648
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679 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
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NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
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                 PIK; A28577; A28577.
HSSP; P16435; 1B1C.
InterPro; IPR001709; FPN_Cyt_redctse.
InterPro; IPR001094; Flavdoxin_like.
PRINTS; PR00369; FLAVODOXIN.
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                                                                                                                                                                                      Conservative 106;
                                                                                                                                          68304 MW;
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(Rel. 30, Last seq
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 NADP+ REDUCTASE,
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426
434
401 AA;
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           REDUCTASE.
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01-0CT-1994
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P37116;
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NON_CONS
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EGGGEEVLIRQYRLLEQPDVQPDRIYTGETARLHSIQNQRPPFDAKNPFLAPIKVNRELH 297
                                                                                                                                                      CPPHKVELEALLEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSIS 832
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"Structural comparison between the trout and mammalian hydrophilic domain of NaDPH-cytochrome P-450 reductase.";

J. Chromatogir A 397:123-136(1987).

-I-FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.

-I- CATALYTIC ACTIVITY: NADPH + 2 ferilcytochrome = NADP(+) + 2
         TLDS--HAGNLPREGAVLIVTASYNGHPPDNAKQFVDWLDQASADEVKGVRYSVFGCGDK
                       NWATTYQKVPAFIDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFNLDI
                                                                ENSEDNKSTLSLQFVDSAADMP-----LAKMH------GAFSTNVVASKELQ
                                                                                                                                         QPGSARSTRHLEIELP-KEASYQEGDHLGVIPRNYEGIVNRVTARFGLDAS----QQIRLE
                                                                                                                                                                                      -----LAKTVSVEELLQYVELQDPVTRTQLRAMAAKTV
                                                                                                                                                                                                    SPE------GKEKYQSWIQDACRNIVHILEDIKSCRPPIDHVCELLPRLQPRYYSIS
                                                                                                                                                                                                                                                                           SSPRVDEKQASITVSVVSGEAWSGYGEYKGIASNYLAELQ----EGDTITCFISTPQSEF
                                                                                                                                                                                                                                                                                         TLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEE
                                                                                                                                                                                                                                                                                                                                LENAQSEGIITLHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQG-AHFYICGDGSQMAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COFACTOR: FAD AND FWN.
SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE
ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
SIMILARITY: THE FWN-BINDING DOMAIN IS RELATED TO BACTERIAL
FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Fragments).
Salmo trutta (Brown trout).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
NCBI_TaxID=8032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R)
                                                                                                                                                                                                                                                                                                                                                                                                           1008 AVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047
                                                                                                                                                                                                                                                                                                                                                                                                                         601 AA
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Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                     730 AEEEKLAHLP------
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(Rel. 17, Last seq
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LYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKKL-IELLDQGAHFYICGD 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 GDKTY-EHYNAMGAYVDKRLEELGAKRVFDLGMGDDGNLEEDFVTWREQFWPAMCEHFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAEEEK------VELQDPVTRTQLR
                                                                                                                                                                                                                                                                                                                                                                                                          SSAPE------GKALYQSFVLEDNRNILAILEDLPSLRPPIDHLCELMPRLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSPSTEQSA -- KKVRKKAENAHNTPLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D----SHAGNLPREGAVLIV--TASY-NGHPPDNAKQFVDWLDQASADEVKGVRYSVFGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 ARYYSIASSSKVHPNSIHICAVLV-----EYXTKGVATTWLKYIR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PQSEFTLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDY
Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1002 GSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047
                                                                                                                                                                                                                           Length 601;
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LeCCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
Phaseolus aureus (Mung bean) (Vigna radiata).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC801767DE1D44C9 CRC64;
                                                                                                                                                                                                                        13.2%; Score 723; DB 1; I
30.2%; Pred. No. 2.8e-33;
iive 106; Mismatches 239;
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293 765 825 397 883 437 943

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1022 QVSEADARLWLQQLEEKGRYAKDVW 1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! - COFACTOR: FAD AND FMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant J. 4:47-60(1993).
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                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                        Shet M.S., Sathasivan K., Arlotto M.A., Mehdy M.C., Estabrook R.W.;
"Purification, characterization, and cDNA cloning of an NADPH-cytochrome P450 reductase from mung bean.";
Proc. Natl. Acad. Sci. U.S.A. 90:2890-2894(1993).
-1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVLIVTASY - NGHPPDNAKQFVDWLDQASADE - - - VKGVRY SVFGCGDKNWATTYQKVPA
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              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
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PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FWN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NALIKKED (ADP PART) (BY SIMILARITY).
N-LIKKED (GLCNAC...) (POTENTIAL).
N-LIKKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                      SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
 Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
PTM: GLYCOSYLATED.
                                                                                                                                                                                         CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome - NADP(+) + 2
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592966167E8561DE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.2%; Score 721; DB
30.6%; Pred. No. 4.4e
Live 109; Mismatches
                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-cv. Berken; TISSUE-Seedling;
MEDLINE-93219390; PubMed-8464904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003097; FAD_binding.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR00126; Flavdoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00258; flavdoxin: 1.
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                                                                                                                                                                                                                   COFACTOR: FAD AND FMN.
Eukaryota; Viridiplantae;
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                                                                                                                                                                                                      ferrocytochrome
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639
275
339
690 AA;
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                                        NCBI_TaxID=3916;
                                                                                                                                                                                                                                                                                                                REDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P00388;
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CARBOHYD
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                                                                                                                                                                    ----PLAKTVSVE-ELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE---KQAY
                                                                                                                                                                                                                                                                                                                                        790 KEQVLAKRLTMLELLEKYPACEMKFSEFI-ALLPSIRPRYYSISSSPRVDEKQASITVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSGEAWSGYGEYKGIASNYL----AELQEGDTITCFISTPQSEFTLPKDPETPLIMVG
    681 TRHLEIELP-KEASYQEGDHLGVIPRNYEGIVNRVTARFGLDASQQIRLEAEEEKLAHL-
                                                                                                                                                                                                                                                      GSLLPPFPGPCSLRTALARYADLLNPPRKAALLALATH-ASEPSDERLKFLSSPQGKDEY
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"Isolation and characterization of a cDNA clone from Catharanthus
"Isolation and characterization of a cDNA clone from expensial
roseus encoding NADPH:cytochrome P-450 reductase, an enzyme essential
for reactions catalysed by cytochrome P-450 mono-oxygenases in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE ER MEMBRANE BY TIS N-TERMINAL HYDROPHOBIC REGION.
SIMILARITY: THE FAN-BINDING DOMAIN IS RELATED TO BACTERIAL FLANODOXINS. THE FAN DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle). Bukaryota: Viridiplantae; Streptophyta; anabryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudioctyledons; core eudiocts; Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NY TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER. TO HEME OXYGENASE AND CYTOCHROME B5.
-i- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADPH-cytochrone P450 reductase (EC 1.6.2.4) (CPR) (P450R).
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Memelink J., Hoge J.H.C.;
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                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S------SYQEGDHLGVIPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  759 VTRTQLRAMAAKTVCPPHKVELEALLE---KQAYKEQVLAKRLIMLELLEKYPACEMKFS
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InterPro: IPR003097; FAD_binding.
InterPro: IPR001099; FPN_Cyt_redetse.
InterPro: IPR0011094; Flavodoxin_like.
InterPro: IPR001226; Flavodoxin_like.
InterPro: IPR001233; Oxred_FAD_NAD(P).
Pfam; PF00175; NAD_binding; 1.
Pfam; PF00567; FAD_binding; 1.
Pfam; PF00667; FAD_binding; 1.
PRINTS; PR00371; FPNCR.
Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
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NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
                                                                                                                                                                                                                                                                       FMN (PYRIMIDINE PART) (BY SIMILARITY)
                                                                                                                                                                                                                                                                               FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
DBDD9AF41374CF91 CRC64;
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                                                                                                                                                                                                                                                                                                                                            Length 714;
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Matches 189; Conservative 118; Mismatches 274; Indels
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                                                                                                                                                                                                                                                                                                                                            12.9%; Score 702;
                                                                                                                                                                                                                                                                                                                         78958 MW;
                                                                                                          EMBL; X69791; CAA49446.1; -. EMBL; Y09417; CAA70571.1; -.
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714 AA;
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HLYFGCRSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGKKLIEL 989
                                     LDQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVW 1046
                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE-93221515; PubMed-7682072;
Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;
Hepatocytes and macrophages express an identical cytokine inducible
nitric oxide synthase gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Karlsen A.E., Andersen H.U., Vissing H., Larsen P.M., Fey S.J., Cuartero B.G., Madsen O.D., Petersen J.S., Mortensen S.B., Mandrup-Poulsen T., Boel E., Nerup J.;
"Cloning and expression of cytokine-inducible nitric oxide synthase Diabetes 44:753-758(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Sprague-Dawley; TISSUE=Astrocytes;
MEDLINE=49.31594; PubMed=7313765;
Galea E., Reis D.J., Felinstein D.L.;
"Cloning and expression of inducible nitric oxide synthase from rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Vascular smooth muscle;

BEDLINE-93191721; Pubmed-7680561;

Nunokawa Y., Ishida N., Tanaka S.;

"Cloning of inducible nitric oxide synthase in rat vascular smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ϋ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              type II)
                                                                                                                                                                                                                                                                                                                                                      NOS2_RAT STANDARD; PRT; 1147 AA. 006518 P97774; 035765; 035766; 064558; 064005; 063267; 01-UDN-1994 (Rel. 29, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 15-UDN-2002 (Rel. 41, Last annotation update) Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, iInducible NOS) (1NOS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Wistar, TISSUE-Pancreatic islets;
MEDLINE-95309542; PubMed-7540573;
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MEDLINE=94325351; PubMed=7519448;
Geng Y.J., Almquist M., Hansson G.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Neurosci. Res. 37:406-414(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eur. J. Biochem. 217:37-43(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN WITHBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY (BY
                                                                                                                                                                                                                                           STRAIN-Dahl/Rapp salt sensitive strain; TISSUE-Vascular smooth muscle;
MEDLINE-98195092; PubMed-9535415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nitric oxide + N NADP(+).
COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FWN. ALSO REQUIRES
TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
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ILSSUE SPECIFICITY: IN NORMAL KIDNEY, EXPRESSED PRIMARILY IN THE MEDULLARY THICK ASCENDING LIMB, WITH MINOR AMOUNTS IN THE MEDULLARY COLLECTING DUCT AND VASA RECTA BUNDLE.

INDUCTION: BY INTERFENO GAMMA AND LIPOPOLYSACCHARIDE (LPS).

SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                               Chen P.Y., Gladish R.D., Sanders P.W., "Vascular smooth muscle nitric oxide synthase anomalies in Dahl/Rapp
 "cDNA cloning and expression of inducible nitric oxide synthase from
                                                                                                                                                                                Sequence analysis of inducible nitric oxide synthase in rat kidney,
                                                                                                                                                                                                                                                                                                                                   STRAIN-Wistar; TISSUE-Renal glomerulus;
Saura M., Zaragoza C., Martinez-Dalmau R., Perez-Sala D., Lamas S.;
"Advances in the studies of NO synthesis regulation in mesanglial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location of an inducible nitric oxide synthase mRNA in the normal
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                                                                                                                                            MEDLINE-97070590; PubMed-8913516;
Tsutsumishita Y., Kawai Y., Takahara H., Onda T., Miyoshi J.,
                                                         Kosuga K., Yui Y., Hattori R., Sase K., Eizawa H., Aoyama Inoue R., Sasayama S.;
Cloning of an inducible nitric oxide synthase from rat polymorphonuclear neutrophils.";
Endothellum 2:217-221(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Sprague-Dawley; TISSUE-Renal glomerulus; MEDLINE-94276509; PubMed-7516453;
                       iochim. Biophys. Acta 1218:421-424(1994).
                                                                                                                                                                                           lung, and uterus.";
Biol. Pharm. Bull. 19:1374-1376(1996).
             muscle cells."
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CALMODULIAN BINDING (POTENTIAL).
FAM (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIGOSE PART) (BY SIMILARITY).
ZINC (BY SIMILARITY).
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                             DNAKQFVDWLDQASADEVKGV----RYSVFGCGDKNWATTYQKVPAF---IDETLAAKGA 594
                                               648 SQLAPTGEGDELSGQEDAFRSWAVQTFR--AACETFDVRSKHCIQIPKRYTSNATWEPEQ 705
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671580 Total number of hits satisfying chosen parameters: 671580 segs, 206047115 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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## SUMMARIES

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-	1736.5	31.8	1066	m	Q9Y8G7	Q9y8q7 fusarium ox
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6	717	13.1	712	10	Q9AU06	Q9au06 populus bal
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proctor R. H., Seo J.-A., Plattner R.D.;
Proctor R. H., Seo J.-A., Plattner R.D.;
Characterization of four clustered and coregulated genes associated
with fumonisin biosynthesis in Fusarium verticillioides.",
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
I- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AF155773; AAG27132.1;
HSSP; P00388; LJ92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1000 GDGSQMAPAVE----ATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVW 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5C6D2B947AE86C25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1462.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro: IPR001128; Cytochrome_P450.
Interpro: IPR001094; FAD binding.
Interpro: IPR001094; Flavdoxin_like.
Interpro: IPR001205; Flavdoxin.
Interpro: IPR001709; FPN_Cyt_redctse.
Interpro: IPR001433; Oxred_FAD/NAD(F).
Pfam; PF00667; FAD binding; 1.
Pfam; PF00658; flavodoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Pezizor
Hypocreales; Nectriaceae; Gibberella
NCBI_TaxID=117187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heme; Monooxygenase; Oxidoreductase
SEQUENCE 1115 AA; 123276 MW; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00175; NAD_binding; 1. PF00067; p450: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00369; FLAVODOXIN. PRINTS; PR00371; FPNCR. PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gibberella moniliformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                              664
                                                                                                                                   704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMYDIAV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVDPV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ::|:| ::| || | | : : :|DPVVYGNDADKFIPERMLDDEFARLNKEYPROWKFPGNGKRACIGRPFAMQESLLAMVVL 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKHFDFE-DHINYELDIKETLILKPEGFVVKAKSKK------IPLGGIPSPSTEQS 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         586 DETLAAKGAENIADRGEAD-ASDDFEGTYEEWRE-HMWSDVAAYFNLDIENSEDNKSTLS 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 VLVEHLTKLPYISAVLRETLRLNSPITAFGLEAIDDTFLGGKYLVKKGEIVTALLSRGHY 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKTIWGDDVEEFRPER----FENPSAIPQHAFKPFGNGQRACIGQQFALHEATLVLGMM 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRPVVIVTASYEGOPPSNAAHFIKWMEDLDGNDMEKVSYAVFACGHHDWVETFHRIPKLV 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425 FONFNFTMTDPNYALEIKQTLTIKPDHFYINATLRHGMTPTELEHVLAGNGATSSSTHNI 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
                                                                                                                      R INCEPTO; IPRO013097; FAD_binding.

R InterPro; IPR0013097; FAD_binding.

R InterPro; IPR0013097; FAD_binding.

InterPro; IPR001094; Flavdoxin._like.

InterPro; IPR001094; Flavdoxin._like.

InterPro; IPR001409; FPN_cyt_redctse.

R InterPro; IPR001409; FPN_cyt_redctse.

R Pfam; PF001667; FAD_binding; 1.

R Pfam; PF00167; FAD_binding; 1.

R Pfam; PF00167; FAD_binding; 1.

R PRINTS; PR00371; FPNCR.

R PRINTS; PR00371; FPNCR.

R PRINTS; PR00386; CYTOCHROME_P450; 1.

R PROSTTE; PS00086; CYTOCHROME_P450; 1.

R Heme; Monooxygenase; Oxidoreductase; Membrane; Electron transport;

W Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP.

R DOMAIN 401 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRALDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 MNKLQRANPDDP--AYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSDDLLTHMLNGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKKVRKKAENAHNTPLLVLYGSNMGTAEGTARDLADIAMSKGF-APQVATLDSHAGNLPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKEACDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       485 KAAANLDAKAGSGKPMAIFYGSNSGTCEALANRLASDAPSHGFSATTVGPLDQAKQNLPE
            COFACTOR: BINDS ONE MOLE EACH OF FAD AND FWN (BY SIMILARITY). SUBCELLUIAR LOCATION: MEMBRANE-BOUND. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 1066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 NADPH-P-450 REDUCTASE.
)7 HEME (BY SIMILARITY).
117925 MW; 6B8123698C2233DBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.8%; Score 1736.5; DB 3 36.8%; Pred. No. 2.5e-100; iive 190; Mismatches 444;
                                                                                          EMBL; AB030037; BAA82526.1;
HSSP; P14779; 1BVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                       P450 FAMILY.
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BINDING
SEQUENCE
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1010 ELEAYETIGLVQVRRAYSRDPSAQDAQGCKYVTDRLGKCRDEVARLWMDGAQVLVCG-GK 1068
                                         QMAPAVEATLMKSYADVHQV-SEADARL----WLQQLEEKGRYAKDVW 1046
                                                           ¥.
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InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR002017; Tubulin.
Pfam; PF00067; P450; 1.
PRINTS; PR00385; P450.
                                                                                                                                                                                                Created)
                                                                                                                                                               PRT;
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                                                                                                                                                                                            01-MAY 2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21, Putative cytochrome P450. SCO0801 OR SCF43.12.
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                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                       Streptomyces coelicolor,
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                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-A3(2)
                                       1004
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Best Local S
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ID Q9RD76
AC Q9RD76;
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                     32;
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                                                                          QRLIKEACDESRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKG
                                                                                                                                             115 YHAMWVDIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQ--PHP
                                                                                                                                                                                                                FITSMVRALDEAMNKLQRANPD-----DPAYDENKRQFQEDIKVMNDLVDKIIADRKA
                                                                                                                                                                                                                                                                                     SGEQSDDLLTHMLNGKDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPH
                                                                                                                                                                                                                                                                                                                                                          VLOKAAEEAARVLVDPVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEY
                                                                                                                                                                                                                                                                                                                                                                                                                            PLEKGDELMVLIPQLHRDKTIWGDDVEEFRPERF - - ENPSAIPQHAFKPFGNGQRACIGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 AVNKDQPLFIVFDSVHRDQSTYGADADEFRPERMIKDGFDKLPPCAWKPFGNGVRACVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QFALHEATLVLGMMLKHFDFEDHTNYELDIKETLTLKPEGFVVKAKSKK-----IPLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKGFAPQVATLDSHA-GNLPREGAVLIVTASYNGHPPDNAKQFVDWLDQASADEVKGVRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KQAYKEQVLAKRLTMLELLEKYPACEMKFSEFIALLPSIRPRYYSISSSPRVDEKQASIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            846 VSVV------SGEAWS---GYG----EYKGIASNYLAELQEGDTITCFISTPQSEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLPKDPETPLIMVGPGTGVAPFRGFVQARKQLKEQG-QSLGEAHLYFGCRSPHEDYLYQE
                                                    2 IKEMPOPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAP-----GRVTRYL-SS
                       Gaps
                     113;
                       Indels
   Pred. No. 4.5e-83;
; Mismatches 439;
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<del>:</del>:
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   33.78;
Best Local Similarity
Matches 380; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-A3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Warren T., Saunders D., Sharr S., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
MEDLINE-97000351; PubMed-8843436;
MEDLINE-97000351; PubMed-8843436;
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete genome sequence of the model actinomycete Streptomyces
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PROSITE; PS00227; TUBULIN; 1.
Heme: Monooxygenase; Oxidoreductase.
SEQUENCE 527 AA; 57741 MW; 4A612C1B7A894780 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 417:141-147(2002).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AL136502; CAB66201.1; -.
Last sequence update)
Last annotation update)
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Pred. No. 4.3e-52;
80; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                              Saunders D.C., Harris D.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
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FVVKAKSKKIPLGG---IPSPSTEQSA--KKVRKKAENAHNTPLLVLYGSNMGTAEGTAR 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378 LAQYASEPSEQEQLHKMASSSGEGKELYLSWVVEARRHILAILQDYPSLRPPIDHLCELL 437
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                                                                                                                                                                 261 QKPPFDAKNPFLAAVTTNRKLNQ-GTERHLMHLELDISDSKIRYESGDHVAVYPANDSTL
                                                                                                                                            552 DQASADEVKGVRYSVFGCGDKNWATTYQKVPA---FIDETLAAKGAENIADRGEADASDD
                                                                                                                                                                                                                                                                                       -----GAFSTNVVASKELQQPGSARSTRHLEIEL-PKEASYQEGDHLGVIPRNYEGI
                                                                                                                                                                                                                                                                                                                                                                                                  320 VNQIGEILGADLDVVMSLNNLDEESNKKHPFPCPTTYRT-ALTYYLDITNP-PRTNVLYE
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                                                                                                 FEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSL---QFVDSA----ADMPLAKMH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVWA 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudotsuga menziesii (Douglas-fir).
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pseudotsuga.
NCBI_TaxID=3357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The molecular characterization of a set of cDNAs differentially expressed during Douglas-fir germination and early seedling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=[MIRB] FRANCO; TISSUE=SEEDLING;
Tranbarger T.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 21, Last annotation updat NADPH-cytochrome P450 reductase (EC 1.6.2.4).
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STRAIN-[MIRB] FRANCO; TISSUE-SEEDLING;
Tranbarger T.J., Misra S.;
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                                                                                                                                                                                                                                    RLIKEACDESRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGY 115
                                                                     HAMMVDIAVQLVQKWERLNAD-EHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFI 174
                                                                                        202 TAMVGTLGYA----QRLNTVPAPLAPWLLRDASRRNAADIAHLNRTVDDLVRERRANGGT 257
                                                                                                                                                                                                                ----SGEQSDDLLTHMLNGKDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFL 280
                                                                                                                                                                                                                                                                                   281 VKNPHVLQKAAEEAARVLVD-PVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDT 339
                                                                                                                                                                                                                                                                                                         457
                                                                                                                                                                                                                                                                                                                                                          340 VLGGEYPLEKGDELMVLIPQLHRDKTIWGDDVEEFRPERFENPSAIPQ--HAFKPFGNGQ 397
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                                                                                                                                          TSMVRALDEAMNKLQRAN----PDDP-AYDENKRQFQEDIKVMNDLVDKIIADRKA----
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"High-red yeast, construction of a novel strain of Saccharomyces
cerevisiae stably exerting high activity of hamster cytochrome P450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-2002 (TrEMBLrel. 20, Last annotation update)
NADPH-cytochrome P450 oxidoreductase.
Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Cricetinae;
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InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001265; Flavdoxin.
InterPro; IPR001126; FPN_cyt_redctse.
InterPro; IPR001433; Oxred FAD/NAD(P).
Pfam; PF00567; FAD_binding; 1.
Pfam; PF00155; Riavdoxin; 1.
Pfam; PF00155; NAD_binding; 1.
PRINTS; PR00159; FlavOxIN.
PRINTS; PR00371; FPNCR.
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Submitted (JAN-1996) to th
EMBL; D83230; BAA11856.1;
HSSP; P00388; 1AMO.
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es 210: Conserv
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NCBI_TaxID=10029;
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Q60451;
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                                                                                                651 KITEKGSYIWNLIAQGGYLYVCGDAKGMARDVHRTLHSIVQEQESVDSTSAEATVKKLQT 710
      592 AIQKSGEKLGPAVLFFGCRNRQMDYIYEDELKSYVENGVLTELVLAFSR-EGATKEYVQH 650
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2020 (TrEMBLrel. 20, Last annotation update)
01-MAR-2020 (TrEMBLrel. 20, Last annotation update)
NADPH-FERRIHEMORROTEIN reductase ATR1 (EC 1.6.2.4).
F22K18.280 OR AT4G24520.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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EMBL, AL035556, CAA23011.1; --
EMBL, AL05561; CAB79362.1; --
EMBL, AL161561; CAB79362.1; --
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Best Local Similarity 29.6%; Pred. No. 5.7e-38;
Matches 196; Conservative 120; Mismatches 257; Indels 89;
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Mayer K.F.X., Schueller C.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
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InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00667; FaD_binding; 1.
Pfam; PF00258; flavodoxin; 1.
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InterPro; IPR003097; FAD_binding
InterPro; IPR01094; Flavdoxin_I
InterPro; IPR011226; Flavdoxin_I
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PRINTS; PR00371; FPNCR.
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711 EGRYLRDVW 719
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SEQUENCE FROM N.A.
STRAIN=[MIRB] FRANCO; TISSUE=SEEDLING;
MEDLINE-2100330; PubMed=11117258;
Tranbarger T.J., Forward B.S., Misra S.;
"Regulation of NADPH-cytochrome P450 reductase expressed during
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SEQUENCE 719 AA; 79653 MW; 4AA9B1FBF5591A3D CRC64;
                                                                                                                                                             Douglas-fir germination and seedling development."; Plant Mol. Biol. 44:141-153(2000).
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PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1
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InterPro; IPR001226; Flavodoxin.
InterPro; IPR001109; FPN_CYL_redctse.
InterPro; IPR002114; HPL_SerP_site.
InterPro; IPR00433; Oxred_FAD_NAD(P).
Pfam; PF00667; FAD_binding; 1.
Pfam; PF00175; NAD_binding; 1.
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STRAIN=[MIRB] FRANCO; TISSUE=SEEDLING;
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Submitted (MAR-2000) to the
EMBL; Z49767; CAA89837.3;
HSSP; P00388; 1AMO.
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                             AD--IAMSKGFAPQVATLDSHAGN-----LPREGAVLIVTASY-NGHPPDNAKQFVDW
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                                                                                                           FEGTYEEWREHMWSDVAAYFNLD-IENSEDNKS-------TLSLQ
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Aplales; Apiaceae; Petroselinum.
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MEDLINE-98070859; PubMed-9405720;
Koopmann E., Hahlbrock K.;
"Differentially regulated NADPH:cytochrome P450 oxidoreductases parsley.";
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EMBL; AF024634; AAB97736.1; -.
HSSP; P00388; 1AMO.
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InterPro; IPR001094; Flavdoxin_like.
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                                                                                                                                                                                                                                                                                                                       449 KSKKIPLGGIPSPSTEQSAKKVRKKAENAHNTPLLVLYGSNMGTAEGTARDLADIAMSKG
                                                                                                                                                                                                                                                                                                                                                                                                            FAP--QVATLDSHA-----GNLPREGAVLIVTASY-NGHPPDNAKQFVDWLDQA--SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        452 VAPRLQPRYYSISSSPRMVPSRIHVTCALVYEKTPTG-RIHKGVCSTWMKNAVSLEESHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSVEPPKLIVPKVEIEDEVDDGKKK------VTVFFGTQTGTAEGFAKAFAEEAKARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                711 VNRVTARFGLDASQQIRLEAEEEKLAHL-----PLAKTVSVEELLQYVELQDPVTRTQ
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                                                                                                                                                                                                                                                                               Gaps
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVW 1046
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                                                                                                                                                                                                                                                                               73;
                                                                                                                                                                                                                                    DB 10; Length 681;
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                         681 AA; 75674 MW; C67AD80E8BAAE0F6 CRC64;
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Cytochrome P450 reductase (EC 1.6.2.4).
                                                                                                                                                                                                                                  13.5%; Score 737.5; DB 10; ilarity 30.7%; Pred. No. 7.4e-38; Conservative 104; Mismatches 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ź
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                 IPR001709; EPN_cyt_redctse.
IPR001433; Oxred_FAD/NAD(P).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
IPR001226; Flavodoxin
                                                     Pfam; PF00667; FALDinding; 1.
Pfam; PF00258; flavodoxin; 1.
Pfam; PF00175; NAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                    Best Local Similarity
Matches 200; Conserv
                                                                                                                                                                     Oxidoreductase.
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                                                                                                                                                                                                                                                                                                                             K--GFAPQVATLDSHAG-----NLPREGAVLIVTASY-NGHPPDNAKQFVDWLDQAS-
                                                                                                                                                                                                                                                                                                                                                RYDKAVFKVLDLDDYAAEDEEYEEKLKKENIAFFFLATYGDGEPTDNAARFYKWFSEGNE
                                                                                                                                                                                                                                                                                                                                                                      556 -ADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDDFEGTYE
                                                                                                                                                                                                                                                                                                                                                                                     238 AWKELLWPELDKILRV----EDNSSTAQSPY---TAAIPQYRVVLTKPEDATHINKSFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAKMHGAFST -----NVVASKELQQPGSARSTRHLEIELP - KEASYQEGDHLGVIPRNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               759 VTRTQLRAMAAKTVCPPHKVELEALLE----KQAYKEQVLAKRLTMLELLEKYPACEMKFS
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                                                                                                                                                                                                                                                                                                                                                                                                                 EWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMP----------
                                       Morant M., Hehn A., Werck-Reichhart D., Lesot A., Pallett K.;

"Exploration and polymophism of the cytochrome P450 reductase family
of genes in wheat.";

Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ303373, CAC633301.1;

InterPro; IPR001094; Flavddxin_like.

InterPro; IPR001094; Flavddxin_like.

InterPro; IPR0011709; FN Coviced_Crap.

InterPro; IPR0011709; FN Coviced_Crap.

Pfam; PF00567; FN Coviced_RAD/NAD(P).

Pfam; PF0058; Flavddxin; 1.

Pfam; PF00175; NAD_binding; 1.
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                              73;
                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                Best_Local Similarity 30.0%; Pred. No. 1.2e-37;
Matches 198; Conservative 115; Mismatches 273; Indels
                                                                                                                                                                                                                703 AA; 77429 MW; 2FCA33AA106E1B36 CRC64;
                                                                                                                                                                                                                                       DB 10;
                                                                                                                                                                                                                                     Score 734.5; DB 1
Pred. No. 1.2e-37;
                                                                                                                                                                                                                                      13.5%;
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PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                      Oxidoreductase
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                                                                                                                                                                                                                                                                                                            A RO D.-K., Douglas C.;

"Functional characterization of cytochrome P450 reductase from the "Functional characterization of cytochrome P450 reductase from the "hybrid poplar (Populus trichocarpa X P. deltoides).";

Inhybrid poplar (Populus trichocarpa X P. deltoides).";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF302498; AAK15261.1; -.

R HSSP; P00388; IAMO.

R InterPro; IPR001309; FAD_binding.

InterPro; IPR001226; Flavodoxin.

R InterPro; IPR00133; Oxredctse.

InterPro; IPR001433; Oxredctse.

InterPro; IPR00143; Oxredctse.

R Pfam; PF00667; FAD_binding; 1.

R Pfam; PF0015; NAD_binding; 1.

R Pfam; PF00175; NAD_binding; 1.

R Pfam; PF00175; PR00301; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIPLGGIP-----SPSTEQSAKKVRKKAENAHNTPLLVLYGSNMGTAEGTARDLADIAM
                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2002 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
NADPH-cytcohrome P450 oxydoreductase isoform 3.
Populus balsamifera subsp. trichocarpa x Populus deltoides.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
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Ro D.-K., Douglas C.;
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                                           AHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEKGRYAKDVW 1046
                                                                          Length 692;
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Mignote-Vieux C., Kazmaler M., Lacroute F., Pompon D.M.;
Submitted (MAY-1992) to the EMEL/GenBank/DDBJ databases.
EMEL; X66016; CA446814-1; -.
R HSSP; P00388; 1AMO.
R InterPro; IPR00199; Flavdoxin.
R InterPro; IPR00126; Flavdoxin.
R InterPro; IPR001226; Flavdoxin.
R InterPro; IPR001226; Flavdoxin.
R InterPro; IPR00126; Flavdoxin.
R InterPro; IPR001709; FPN_CYL_redctse.
R InterPro; IPR001173; Oxred_FAD_NAD(P).
R Pfam; PF00667; FAD_binding; 1.
R Pfam; PF00667; FAD_binding; 1.
R Pfam; PF00679; MAD_binding; 1.
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01, Last sequence update)
20, Last annotation update)
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PRINTS; PR00371; FPNCR.
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                                                            PLGVFFAAIAPRLQPRYYSISSCQDWAPSRVHVTSALVYGPTPTG-RIHKGVCSTWMKNA 513
                                                                                                                                                                                                                                                      926 SLGEAHLYFGCRSPHEDYLYQEELENAQSEGIIT-LHTAFSRMPNQPKTYVQHVMEQDGK 984
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                                                                                                                                                              470 VRKKAENAHNTP----LLVLYGSNMGTAEGTARDLAD--IAMSKGFAPQVATLDSHAG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98005363; PubMed-9434750; Rosco A., Pauli H.H., Priesner W., Kutchan T.M.; Rosco A., Pauli H.H., Priesner W., Kutchan T.M.; "Cloning and heterologous expression of NADPH-cytochrome P450 reductases from the Papaveraceae."; Arch. Biochem. Biophys. 348:369-377(1997). EMBL; U67185; AACCO021.1; -...69787; P00388: 1AMO.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 05, Last annotation update)
NADPH:ferrihemoprotein oxidoreductase (EC 1.6.2.4).
Papaver somniferum (Opium poppy).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales; NCBI_TaxID=3469;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HASSY; WOOSO; ALW.;
InterPro; IPR001094; FAD_binding.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001226; Flavodoxin.
InterPro; IPR001709; FPN_Cyt_redctse.
InterPro; IPR001709; FPN_Cyt_redctse.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00657; FAD_binding; 1.
Pfam; PF000588; Ilavodoxin; 1.
Pfam; PF00175; NAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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694 326 747 368 786 428 845 488

211

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960 -LHTAFSRMPNQPKTYVQHVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYA 1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           900 MVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGIIT 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | |||| | | ||| | | ||| || 606 ELIVAFSREGPQ-KEYVQHKMVDRAAEIWTIISQGGYFYVCGDAKGMARDVHRTLHTIVQ 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-VAR. LOLITA; TISSUE-SEEDLING; Benveniste I., Begue-Kirn C., Lesot A., Hasenfratz M., Durst F.; "Isolation and characterization of a cDNA encoding an NADPH-cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 491 GTAEGTARDLAD--IAMSKGFAPQVATLDSHA-----GNLPREGAVLIVTASY-NGHP
                                                                      541 PDNAKQFVDWLDQASADEV - - KGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIA
                                                                                                                                                                           212 PVGLGDDDQCIEDDFSAWKEFLWPELD----QLLRDEDDVNAPSTPYTAAIPEYRLVIH
                                                                                                                                                                                                                                                267 DPSIISVEDKFSNLANGNVSFDIHHPCRVNVAVQKELHKAESDRSCIHLEFDITGTGITY
                                                                                                                                                                                                                                                                                                                     ETGDHLGVYAENSDETVE-------EAGKLLDKPLDLLFSIHADNEDGT
                                                                                                                                                                                                                                                                                                                                                                                            369 AIGSSLPPPFFGPCTLHTALACYADLLSPPKKAALLALAAHASEPSEADRLKFLSSPQGK
                                                                                                                                                                                                                                                                                                                                                                                                                               787 QAYKEQVLAKRLTMLELLEKYPACEMKFSEFI-ALLPSIRPRYYSISSSPRVDEKQASIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vicia sativa (Spring vetch) (Tare).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Vicia.
                                   GTAEGFAKALAEEVKARYEKAAVKVFDLDDYAMEDDQYEEKLKKETLALFMVATYGDGEP
                                                                                                                                         599 DRGEADASDDFEGTYEEWREHMWSDVAAYFNLDIENSEDNKSTLSLQFVDSAADMPLA--
                                                                                                                                                                                                              695 QEGDHLGVIPRNYEGIVNRVTARFGLDASQQIRLEAEEEKLAHLPLAKTVSVE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P450 reductase from Vicia sativa.";
Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
EMBL: 22652; CAA81211.1; -
HSSP: P00388; 1J92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-1906 (TrEMBLrel. 21, Last annotation update)
NADPH-ferrihemoprotein reductase (EC 1.6.2.4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQGGLDSSKTESMVKKLQMEGRYLRDVW 692
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InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00667; FAD_binding; 1.
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InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001226; Flavodoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 431 LDIKETLTLKPEGFVVKAKSKKIPLGGIPSPSTEQSAKKVRKKAENAHNTPLLVLYGSNM 490
                                                                                                                       EEKLAHLPLAKTVSV-----EELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEA 782
                                                                                                                                                                                                            897
                                                                                                                                                                                                                                                                                 LIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQSEGI 957
60 LVVPKSLSIKDE-----EDESEALGG------KTKVTIFYGTQT 92
                                                                        : | :: | | : | | DGS----PQGSSLPPFFPGPCTLRSALARYADLLNPPRKASLIALSAHASVPSEAERLRF
                                                                                                                                                                                          L---LEKQAYKEQVLAKRLTMLELLEKYPACEMKFSEFI-ALLPSIRPRYSISSSPRVD
                                                                                                                                                                                                                                                               EKQASITVSVVSGEAWSGYGEYKGIASNYLAELQEGDT-ITCFISTPQSEFTLPKDPETP
                                                                                                                                                                                                                                                                                                                                                          PGSARSTRHLEIELP-KEASYQEGDHLGVIPRNYEGIVNRVTARFG--LDASQQIRLEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
NADPH-cytochrome P450 oxgloreductaee isoform 1.
Populus balsamifera subsp. trichocarpa x Populus deltoides.
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids 1; Malpighiales; Salicaceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ro D.-K., Douglas C.;
"Functional characterization of cytochrome P450 reductase from the hybrid poplar (Populus trichocarpa X P. deltoides).";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF302496; AAK15259.1;
HSSP; P00388; 1AMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.0%; Score 711.5; DB 10; Length 692; ilarity 28.9%; Pred. No. 3.3e-36; Conservative 110; Mismatches 252; Indels 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76725 MW; 7AA8CC78B3C984D9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : : | ::|| :||| 654 AQEQGPMESSAAEAAVKKLQVEERYLRDVW 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           naser, rousos, rass.
InterPro; IPR001094; FAD_binding.
InterPro; IPR001206; Flavdoxin_like.
InterPro; IPR001206; Flavodoxin.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR001433; oxred_FAD/NAD(P).
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Pfam; PF00258; flavodoxin; 1.
Pfam; PF00175; NAD_binding; 1.
PRIWTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 APQRVHVTCALVEGPTPTG-RIHKGVCSTWMKSATPLEKSHDCSRAPIFIRPSNFKLPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          894 PETPLIMVGPGTGVAPFRGFVQARKQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELENAQ
                                                                                                                                                                                                                                                                 106 ALHEATLVLGMMLKHFDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGIPSPSTEQ
                                                                                                                                                                                                                                                                                               ----GNLPREGAVLIVTASY-NGHPPDNAKQFVDWLDQASADE---VKGVRYSVFGCGDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NWATTYOKVPAFIDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFNLDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAEEEKLAHL-----PLAKTVSVEELLQ-YVELQDPVTRTQLRAMAAKTVCPPHKVELE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                782 ALLE----KQAYKEQVLAKRLTMLELLEKYPACEMKFSEFI-ALLPSIRPRYSISSSPRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEKQASITVSVVSGEAWSGYGEYKGIASNYLAEL----QEGDTITCFISTPQSEFTLPKD
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Triticum.
                                                                                                                                                                                                                       92;
                                                                                                                                                                   Length 692;
                                                                                                                                                                                                                       Indels
                                                                                                                      49CB4AEC8611BE99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMKSYADVHQVSEAD --- ARLWLQQLEEKGRYAKDVW 1046
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Last annotation update)
                                                                                                                                                                   13.0%; Score 711; DB 10; 28.4%; Pred. No. 3.5e-36;
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01-WAR-2002 (TrEMBLrel. 20, Last annotation
NADPH-cytochrome P450 reductase (Fragment).
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Pfam; PF00258; flavodoxin; 1.
Pfam; PF00175; NAD_binding; 1.
PRINTS; PR00369; FLAVODOXIN.
PRINTS; PR00371; FPNCR.
                                                                                                                      692 AA; 76912 MW;
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                                                                                           Oxidoreductase.
                                                                                                                                                                                            tal Similarity
198; Conserv
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                                                                                                                    SEQUENCE
                                                                                                                                                                      Query Match
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Matches
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MEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLEEK 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 ARYEKVLFKVVDLDDYAAEDDEYEEKLKKETFALFFLATYGDGEPTDNAARFYKWFTEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 EKEVWLKDFNYAVFGLGNRQY-EHFNKVAKEVDELLLEQGGNRLVPCGLGDDDQCIEDDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              653 MPLAKMHGAFS-----TNVVASKELQQPGSARSTRHLEIELPKEA-SYQEGDHLGVIPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     756 ODPVTRTQLRAMAAKTVCPPHKVELEALLE---KQAYKEQVLAKRLTMLELLEKYPACEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 LNAPKKAALTALAAHASDPTEAERLRFLASPAGKDEYAQWIVASQRSLLEVMAAFPSAKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SK--GFAPQVATLDSHAG-----NLPREGAVLIVTASY-NGHPPDNAKQFVDWLDQAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        614 EEWREHMWSD-----CAPAYFNLDIENSEDNKSTLSLQFVDSAAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 TAWKELVWPELDQLLRDEDDTTGATTPYTAAIPEYRVVFIDKSD------LEFEDKS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        706 NYEGIVNRVTARFGLDASQQIRLEAEEE-----KLAHLPLAKTVSVE-ELLQYVEL
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                                                            Ξ.
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                                                            Schaller
                                                                                                                   "Increasing expression of P450 and P450-reductase proteins from monocots in heterologous systems.";
Arch. Blochem. Biophys. 379:161-169(2000).
EMBL; AF123610; AAG17471.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 656;
                                                            Batard Y., Hehn A., Nedelkina S., Schalk M., Pallett K.,
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13.0%; Score 710; DB 10;
Best Local Similarity 29.5%; Pred. No. 3:7e-36;
Matches 197; Conservative 109; Mismatches 264;
                                                                                                                                                                                                                                                                   InterPro; IPR003097; FAD_binding.
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001226; Flavdoxin_like.
InterPro; IPR0011709; FPN_CYL_redctse.
InterPro; IPR0011709; FPN_CYL_redctse.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF0055; FAD_binding; 1.
Pfam; PF00175; NAD_binding; 1.
STRAIN-CV. DARIUS;
MEDLINE-20322901; PubMed-10864454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00369; FLAVODOXIN
PRINTS; PR00371; FPNCR.
                                                                                         Werck-Reichhart D.;
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-- AAYFNLDIENSEDNKSTL 642

693

403 802

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977 HVMEQDGKKLIELLDQGAHFYICGDGSQMAPAVEATLMKSYADVHQVSEADARLWLQQLE 1036
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                                                                                                                                                                                                                                                                                                                                                                                                              918 KQLKEQGQSLGEAHLYFGCRSPHEDYLYQEELEN-AQSEGIITLHTAFSRMPNQPKTYVQ 976
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------DINMANGNGYTVFDAQHPYKANVAVKRELHTPESDRSCIHLEFDIAGSGLT
                                          236 LGDDDQCIEDDFTAWREALWPELDTILREEGDTAVATPYTAAVLEYRVSIHDSEDAKEN-
                                                                                643 SLQFVDSAADMPLAKMHG-----AFSTNVVASKELQQPGSARSTRHLEIELPKEA-S
                                                                                                                                                                            346 YETGDHVGVLCDNLSETVDEALRLLDMSPDTYFSLHAEKED--GTPISSSLPPPFPPCNL
                                                                                                                                                                                                              747 -EELLQYVELQDPVTRTQLRAMAAKTVCPPHKVELEALLE---KQAYKEQVLAKRLTMLE
                                                                                                                                                                                                                                                                               LLEKYPACEMKFSEFIA-LLPSIRPRYSISSSPRVDEKQASITVSVVSGEAWSGYGEYK
                                                                                                                                             694 YQEGDHLGVIPRNYEGIVNRVTARFGLDASQQIRLEAEFEKLAHLPLAKTVSV-----
                 602 EADASDDFEGTYEEWREHMWSDV----
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                                                                                                                                                                                                                                                                                                                          Bevan M., Kalicki J., Wohldmann P., Smith A., Bancroft I., Mewes H.W.,
Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                          F9N11.60 OR AT4(330210.
Arabidopsis thaliana (Mouse-car cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brasslcales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SOUTHWICK A., Karlin Neumann G., Nguyen M., Lam B., Miranda M.,
Palm C.J., Theologis A., Ecker J., Davis R.W.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL109796, CAB52465.1;
EMBL, AL1057576; CAB81014 1;
EMBL, AZ525101; AAK17169.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Smith A., Mewes H.W., Lemcke K., Malicki J. Wohldmann P., Smith A., Mewes H.W., Lemcke K., Mayer R.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis sequencing project;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
NADPH-FERRIHEMOPROTEIN reductase (ATR2) (EC 1.6.2.4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.0%; Score 709; DB 10; 28.4%; Pred. No. 4.9e-36;
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InterPro; IPR001205; Flavdoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P)
Pfam: PF00667; FAD_Binding; 1.
Pfam: PF00258; flavodoxin; 1.
Pfam: PF00175; NAD_binding; 1.
                                                                                              PRT;
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PRINTS; PR00371; FPNCR.
                                                                                              PRELIMINARY;
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GRYLRDVW 656
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Best Local S
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